### U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

S	SEARCH REQUEST FORM			
Requestor's Name:	h S BASI Number: 091	462 4	-116	,
Date: 12/6/01	Phone: 3089475 Art I Rm 10E17 mai/rum 1000 Intelantin 6 sofuthe la	Unit:	46	
Please write a detailed statement of search that may have a special meaning. Give exa	In telantin 5 which (a topic. Describe specifically as possible the subject matter amples or relevant citations, authors keywords, etc., if known a copy of the broadest and/or most relevant claim(s).	to be searched.	Define any terms	
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	Point of Contact: Toby Port Technical Info. Specialist CM1 1E0T TEL: 308-3534 12C/4			
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ALIGNMENTS

## hepatotoxic agent protection; neurological disorder. Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6; chimeric protein; fusion protein; cell growth inhibitor; melanoma cell; highly malignant cancer cell; in vivo engraftment; mammalian cancer; human haematopoietic cell; bone marrow transplantation; mammalian cancer; hepatotoxic agent protection; haematopoiesis; liver disorder; Synthetic. AAY03165; AAY03165 standard; protein; 21-JAN-1999 WO9902552-A2 Linker used in Chimeric sIL-6R/IL-6 protein. 11-JUN-1999 (first entry) 13 A

10-JUL-1997; 30-DEC-1997; 97IL-00121284. 97IL-00122818.

09-JUL-1998;

98WO-IL000321.

(YEDA ) YEDA RES & DEV CO LTD.

WPI; 1999-120776/10.

Revel M,

Chebath J,

Lapidot T,

Kollet 0;

New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for e.g. treating cancers, bone marrow transplantation, increasing haematopoiesis or treating liver or neurological disorders.

Claim 5; Page 54; 77pp; English.

This sequence represents a linker that can be used in the chimeric glycosylated soluble interleukin-6 receptor (sIL-6R)-interleukin-6 (IL-6) protein (sIL-6R)-interleukin-6 the invention. The SIL-6R/IL-6 protein comprises a fusion protein product between all of the naturally occurring form of sIL-6R and all of the naturally occurring form of independent of the naturally occurring form of IL-6, the sIL-6/IL-6 and analogues being glycosylated in a similar fashion to the glycosylation of naturally occurring sIL-6R and IL-6. The sIL-6R/IL-6 and analogues are capable of inhibiting the growth of highly malignant cancer

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                                         The invention describes the use of interleukin-18 (II-18) inhibitor for manufacture of medicament for treatment and/or prevention of diseases or diseased conditions of the arteries, heart failure recurrent events, or as diagnostic marker for bad clinical prognosis in heart failure or recurrent events after first event of heart failure. The II-18 inhibitor is useful for: the manufacture of a medicament for treatment and/or prevention of atherosclerosis/arteriosclerosis/ the manufacture of a medicament for treatment and/or prevention of trombosis of atherosclerotic plaque (AP), AP ulcer, AP destabilisation (responsible for stroke), atheroma, isohaenic syndromes e.g. myocardial infarction, Al disminishment and failure recurrent summits of death recurrent.
disruption or heart failure recurrent events e.g. death, recurrent ischaemia, re-vascularisation and progression of atherosclerosis, the heart failure is ischaemic or non-ischaemic and as a diagnostic
                                                                                                                                                                                                                                                                                    Use of interleukin-18 inhibitor for manufacture of medicament for treatment and/or prevention of atherosclerosis, thrombosis of atherosclerotic plaque, atherosclerotic plaque ulcer and heart failure
                                                                                                                                                                                                                                                   Disclosure; Page 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin 18; II-18; cytokine; interleukin-18 inhibitor; atherosclerosis; cardiant; vasotropic; antiulcer; myocardial infarction; atherosclerotic plaque; thrombosis of atherosclerotic plaque; stroke; ischaemic syndrome; heart failure; arteriosclerosis; vascularisation; atheroma; immunoglobulin; linker peptide.
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The present invention relates to the use of human secreted apoptosis-
CC related protein 1 (SARP-1), SARP-1 nucleic acids and/or a substance which
CC stimulates the release or potentiates the activity of endogenous SARP-1
CC initiates signalling of the human SARP-1 receptor. The SARP-1 protein binds to and
CC initiates signalling of the human SARP-1 receptor. The SARP-1 protein can
CC SARP-1 can be used in gene therapy. And the polymucleotide sequences encoding
CC sequences, and pharmaceutical compositions comprising SARP-1 are useful
CC for the treatment of scleroderma, especially systemic sclerosis. They may
CC interstitial pulmonary fibrosis, Dupuytren's contracture, keloid and
CC reactive fibrosis), chronic heart failure (particularly after myocardial
CC infarction), disorders involving inflammation of the lung (e.g. rheumatoid
CC arthritis). The present sequence represents a linker peptide that can be
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nucleic acid
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17-AUG-2001;
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sis; systemic disease;
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                                                                                                                                                                                         The invention relates to the use of a substance (I) signaling through gpl30, or use of a vector (II) for inducing and/or enhancing the endogenous production of interleukin-6 (II-6) in a cell. (I), (II) or a cell expressing (I), is useful in the manufacture of a medicament for the treatment and/or prevention of diabetic neuropathy. (I) is useful for treating or preventing diabetic neuropathy such as polyneuropathy or mononneuropathy. The present sequence represents a linker peptide used for
           AAY25368
                                                                                                                                                          Sequence 13
                                                                                                                                                                                                                                                                                    Disclosure; Page 17; 85pp; English.
                                                                                                                                                                                                                                                                                                                    Use of a substance signaling through gp130, or use of a vector for inducing and/or enhancing endogenous production of interleukin-6 in for preparing a medicament for treating and preventing diabetic
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-403150/38.
                                                                                                                                                                                                                                                                                                                                                                                         Dreano M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003033015-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               II-6; gp130; interleukin-6; antidiabetic; neuroprotective; gene therapy;
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                                                                                                                                                                                 IL-6R/IL-6 chimera
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Matches 13; Conserv
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IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral; human interferon alpha/beta receptor; anticancer; immunomodulatory; anti-arthritic; antidiabetic; treatment; hepatitis, viral infection; hairy cell leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus;
                                                                                                               06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prolonging in vivo activity of type I interferon
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                                                                               IFNAR2/IFN-beta complex peptide fragment 12.
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Pred. No. 0.00074;
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Matches 13
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                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                     Bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa polypeptide #2338.
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                                                    18-FEB-1998;
27-JUL-1998;
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     (GENO-) GENOME
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     THERAPEUTICS CORP
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa infection; antibacterial
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Pred. No. 0.0
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                                                                                                                                                                                         The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and continuous as molecular targets for diagnostics, therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa mucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, concluding anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused components for diagnosis and/or treatment of P. aeruginosa-sequences AB667826-CAB084396 represent P. aeruginosa-polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                Matches
                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                  Sequence 360 AA;
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    3 GAGLVLGGQF
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8; Conserv
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RRESULT 8
AAY37561
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XX MO99
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PD 10-J
PD 11-J
PR 04-N
XX 28-N
PR 17-D
PR 04-N
XX 28-N
PR 17-D
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17-DEC-1997;
04-NOV-1998;
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nongonococcal uretritis; epidymitis; cervicitis; salpingitis;
bartholinitis; pneumopathy; venereal lymphogranulomatosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein involved in intermediate metabolism of fatty acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY37561 standard; protein; 199
                                             WPI; 1999-371125/31.
                                                                                                                                     Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis
                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
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                                                                                                                                                                                                                                                                                                                                                            97FR-00015041.
97FR-00016034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-IB001939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conventional trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nonendemic trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            perihepatitis;
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Disclosure; Page 1221; 1755pp; English

**sequence** 

of Chlamydia trachomatis

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RESULT 9
ADM98607
ID ADM9
XX ADM9
AC ADM9
XX ADM9
XX Gera
XX Gera
XX Gera
XX Gera
XX Poll
XX Poll
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                                                                                   The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence encoding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in the organism. The invention also relates to methods of producing a time organism.
                                                                                                                                                                                                                                                                                                                                                                     New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JAN-2002; 2002US-00041018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geranylgeranyl pyrophosphate synthase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-2004
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diterpene or diterpene precursor and a method of isolating a diterpene synthase comprising growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-2001; 2001US-0259880P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004072323-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGAGLVLGGQF 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attractant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                  IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hart EA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                               27; 38pp;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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88888888888888888
                                                                              the cells further comprises at least one isolated and purified nucleic card sequence of a yeast expression library, and the expression of the nucleic acid sequence is regulated by an inducible promoter under conditions where the expression is induced, filtering the cell/resin card extracting the cell/resin mixture with alcohol to produce an companic eluent and analysing the organic eluent by a screening method corganic eluent and analysing the organic eluent by a screening method card sequence encoding the diterpene synthase. The unicellular card sequence encoding the diterpene or diterpene precursor producing system. Diterpenes, in plants, serve as defence toxins, volatile confensive signals, pollinator attractants and photoprotectants. This sequence represents a geranylgeranyl pyrophosphate synthase polypeptide of the invention. Note: The sequence data for this patent did not form the printed specification but was obtained in electronic format
Sequence 291 AA;
                                                              USPTO at
                                                           seqdata.uspto.gov/sequence.html.
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Matches
                                      Query Match
Best Local
153
                N
                                       Similarity
               FGAGLVLGGQF 12
FGVGGILGGQY 163
                                Conservative
                                      61.2%;
                                ?
                                        Score 41;
Pred. No.
                                Mismatches
                                        .8e+02;
                                Indels
                                0
                                Gaps
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DB 8;

Length 291;

0

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RESULT 10
ABR53138
ID ABR53
XX ABR53
XX ABR53
XX ABR53
XX Prote
XX Multi
XX Multi
XX Sacch
XX FP125
XX FP125
XX FP15-MF
XX CELL
XX WPI,
PI Marz:
XX WPI,
DR W-PSI
DR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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15-MAY-2001; 2001EP-00111774. 20-DEC-2001; 2001EP-00130253.

(CELL-) CELLZOME AG

Bauer A,

Z,

Gavin A, (

Grandi P,

ďĎ,

Superti-Furga GD;

Krause R,

Kruse

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Kuester

N-PSDB; 2003-250078/25. ACC61180

New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of diseas of disease ç

SEQ ID NO 1141; 17pp + Sequence Listing; English

The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this

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RESULT 11
ADK63100
ID ADK633
XX ADK63
XX D16ea
X
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                    hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bauer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disease treating protein complex-derived protein #676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel protein complexes comprising a first and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 1351; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marzioch M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-DEC-2001; 2001EP-00130253
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DB; ADK63101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein, or its derivative, fragment, homologue or variant. The are selected from given protein complexes, which are not defined specification. The variants are encoded by nucleic acids that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EFGAGLVLGGQ 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superti-Furga G, Kuester B, Schu. P, Krause R, Kruse U, Merino A, C, Rick J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%;
63.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schultz J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bauch A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Sequence 623

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FAAGLALGGQ

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RESULT 12
ABO7896
AD ABO789
AXX ABO78
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AXX CENC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                         The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and contered therefore the respect for diagnostics, by rophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, conformed the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, concluding anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-calerived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caleed components for diagnosis and/or treatment of P. aeruginosa-caleed components for diagnosis and/or treatment of P. aeruginosa-sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed consideration but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 7
                                                                   Matches
                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 27542; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa polypeptide #10971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2004
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                                                                                                                                                                                                                                               seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME
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         2 FGAGLVLGGQ 11
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7; Conserv
                                                               Similarity
8; Conserv
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                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0074788P
98US-0094190P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nolling J,
                                                                                               61.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.2%;
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Pred. No.
                                                                                               Score 41;
Pred. No.
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                               4.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                            Length 640;
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RESULT 13
AAB66456
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Best Local S
Matches 10
                                                                                                                                                                isolating mutants of actinomycetales and for identifying compounds that have antibiotic activity. The method is used to identify mutants of microorganisms, preferably an actinomycetales, such as M. tuberculosis, M. bovis, M. leprae, M. avium, M. intracellulaire and M. paratuberculosis, that is unable to grow under specific conditions. It is especially useful for identifying loci involved in pathogenicity. It is useful in constructing vaccines. The method can be used to screen multiple libraries concurrently. It can screen libraries of different organisms or different strains of the same organism. The present protein is encoded by a gene which is disrupted by the insertion of the IS 1096 transposon to produce an attenuated mutant of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening a mutant library for mutants unable to grow under specific conditions and for identifying loci involved in pathogenicity, comprises using signature tagged transposon mutagenesis.
                                                                                                                                                                                                                                                                                                                                                             treating an individual suffering from a mycobacterial infection, suspected of being infected with a Mycobacterium, or having been exposed to an infectious Mycobacterium. It is also useful for identifying and
                                                                                                                                                                                                                                                                                                                                                                                                              library with insertions in genes and/or regulatory regions of the organisms of interest, where the insertion contains a tag and/or a transposon associated with a tag. The mutants are identified by hybridisation of the tags to known sequences. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gicquel B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signature tagged transposon mutant; mutant library;
mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
                                                                                                                                     Sequence 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is given in a specification relating to a method screening a library of mutants. The method comprises constructing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Fig 14A; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-2000; 2000WO-IB000950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200102555-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis; attenuated microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Mycobacterium tuberculosis mmpL7 (Rv2942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-2001
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)B; AAF31617.
876
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                                  N
                                                                                    Similarity
FGAGLVLVSGGSF 888
                                FGAGLVL--GGQF 12
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guilhot C,
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99US-0142833P
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                                                                                  61.2%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Camacho
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                                                                Score 41; DB
Pred. No. 6e+0
0; Mismatches
                                                                  0
                                                                                  DB 4;
6e+02;
                                                                                                 Length 920;
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RESULT 14

Propionibacterium acnes

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Matches 10
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                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated mycobacterial peptides, useful for the manufacture medicament for treating or preventing a mycobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                James BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mycobacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of gene down-regulated during nutrient starvation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR55195 standard;
                             dermatological; osteopathic; neuroprotectant.
                                                                                                   Propionibacterium acnes immunogenic protein #12872.
                                                                                                                                  27-FEB-2002
                                                                                                                                                             AAU51976;
                                                                                                                                                                                          AAU51976 standard;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 920 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ACC43891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-2001; 2001GB-00025535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-OCT-2002; 2002WO-GB004718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carbon starvation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-2003
                                                                                                                                                                                                                                                                  876 FGAGLVLVSGGSF 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                            2 FGAGLVL--GGQF 12
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 117-121; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marsh P,
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; transmembrane transport protein MMPL7
                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nutrient-starving culture; mycobacteria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 920
                                                                                                                                                                                                                                                                                                                                        61.2%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hampshire
                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                         Score 41; DB
Pred. No. 6e+0
0; Mismatches
                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                        6e+02;
                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                                      Length 920;
                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 16
ABM48495
ID ABM48
 BXSXXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

C. P. acnes is also involved in infections of bone, joints and the central corrous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the correct or absence of P. acnes in a patient comprises contacting a compression of a binding agent that binds to the proteins of the invention compression of antibodies conficted and determining the amount of bound protein in the sample. The correction of antibodies specific for P. acnes proteins. These antibodies can be used to compression and activity of P. acnes polypeptides and compression across presence, for example, by constituted immunosorbent assay (ELISA). Note: The sequence data for cobtained in electronic format directly from WIPO at the printed specification, but was constant of the printed specification, but was constant of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                 Propionibacterium acnes predicted ORF-encoded polypeptide #13171
WO2003033515-A1
                                                                                                                                                                                                                                  ABM48495 standard; protein; 57
                                Propionibacterium
                                                             Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                              20-OCT-2003
                                                                                                                                                                                                   ABM48495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides. The proteins and their associated DNA sequences are the treatment, prevention and diagnosis endical conditions cape across. The disorders include SAPHO syndrome (synovitis, acros, pustulosis, hypertosis and osteomyelitis). uveitis and endornthis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 13171; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes vaccinating against and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW, Persing DH,
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US012865.
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                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                             43
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                                                                                                                                                                                                                                                                                                                                                            FGAGLVLGGQ 11
                                                                                                                                                                                                                                                                                                                            FGAGLVYAGQ 52
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                           (first entry)
                                acnes
                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides and nucleic acids useful for diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 57;
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                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 17
ABO83978
ID ABO83
XX
AC ABO82
XX
DT 29-J1
XX
DE Pseu
XX
KW Bact
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC encoding a Propionibacterium acres polymetrice (ACTev433-ACTEV433) or polymeptides encoded by the polymucleotides (ARM35624-ARM64536) and to CC immunogenic fragments of P. acres polypeptides. The invention also relates to CC immunogenic fragments of p. acres polypeptides. The invention of CC additionally encompasses expression vectors and host cells comprising a CC polymucleotide of the invention; antibodies against polypeptides of the invention; a cell polypeptide of the invention; a comprising a polypeptide of the invention; a cC polypeptide and an isolated T cell population comprising T cells prepared CC via this method; a vaccine composition (comprising P. acres polypeptides, cC polymucleotides, antibodies, fusion proteins, T cell populations, or CC antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acres in a cC patient; and a method for inhibiting the development of P. acres in a cc patient; and a method for inhibiting the development of P. acres in a cc patient; and a method for inhibiting preventing cells that express the creating. The P. acres polypeptides, polymucleotides, antibodies, fusion proteins. Toell populations or antigen-presenting cells that express the collypeptides are useful for diagnosing, preventing or treating acres collypeptides are useful for diagnosing, preventing or treating acres collypeptides are useful for diagnosing, preventing or treating acres collection. The polymucleotides can also be used as probes or primers for mulation of an immune response against P. acres, or for treating acres, and the kit is useful for prevention. The present sequence can also be used as probes or primers for composition of an immune response against P. acres, or for treating acre, and the kit is useful for prevention. The present sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly composition is patent did not format directly from WiPo at ftp. 
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitcham JL,
Zhang Y, Wa
Barth B, Va
                                                              Pseudomonas aeruginosa polypeptide #16153.
                                                                                                          29-JUL-2004
                                                                                                                                                    AB083978;
                                                                                                                                                                                        ABO83978 standard; protein; 171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 13171; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-381789/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2003
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                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                  Similarity 80.88; Conservative
                                                                                                                                                                                                                                                                                                  FGAGLVYAGO
                                                                                                                                                                                                                                                                                                                                        FGAGLVLGGQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang S, Jen S, Lod
Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW,
ang S, Jen S,
                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                      59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                          6
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 57;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

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RESULT 18
ABM65541
ID ABM65
XX ABM65
XX ABM65
XX ABM65
XX ACOC
DT 20-OC
DT 20-OC
DT ACOC
DT 20-OC
DT 20-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosis and CC therapy of pathological conditions, as molecular targets for diagnostics, CC prophylaxis and treatment of pathological conditions resulting from a CC bacterial infection, for evaluating a compound, such as a polypeptide, CC for the ability to bind a P. aeruginosa nucleic acid, as components of CC effective antibacterial targets, as targets for antibacterial drugs, CC including anti-P. aeruginosa drugs, as templates for recombinant CC production of P. aeruginosa-derived peptides or polypeptides, as target CC components for diagnosis and/or treatment of P. aeruginosa-caused CC infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using blochip technology. Sequences ABO67826-CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence date for this patent did not form part of the printed CC specification but was obtained in electronic format from USPTO at CC sequence date for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                 11-OCT-2002; 2002WO-US032727
                                                                                               24-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic polypeptide #30217
                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM65541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM65541 standard; protein; 406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 171 AA;
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27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
                                                                                                                                                                                                                      Propionibacterium
                                                                                                                                                                                                                                                                                  immunostimulant; immune response; vaccine; immunogenic
                                                                                                                                                                                                                                                                                                                   Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.7%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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27-SEP-2001

WO200171042-A2

Drosophila melanogaster

pharmaceutical

Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster polypeptide SEQ ID NO 12009

26-MAR-2002

(first entry)

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                                                                                                                                                                                                                                                                                                                                            RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polynucleotide (ACF64435-ACF64733) CC encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention CC additionally encompasses expression vectors and host cells comprising a polypucleotide for stimulating an immune response specific for a P. acnes convention; antibodies against polypeptides of the invention; a comprising a polypeptide for a P. acnes convention; a comprising p. acnes polypeptides, antibodies, fusion proteins comprising P. acnes polypeptides, comprising p. acnes in a complex present present of p. acnes in a complex present present of p. acnes in a complex present present of p. acnes in a complex present present present of p. acnes in a comprising, comprising p. acnes in a complex present pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                              ABB61739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 406 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-381789/36
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                                                                                                                                                                                                                                                                                                      ABB61739 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                      392
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      FGAGLVYAGO
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Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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ng S, Jen S,
                                                                                                                                                                                                                                                                                                    protein; 805
                                                                                                                                                                                                                                                                                                                                                                                                      401
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
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Jones R, Carter D;
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XX M Mitco
KW Hunti
KW Lebeel
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Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB018737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the sequences of the sequence data for this patent did not format directly are the sequence of the sequence data for this patent did not format directly part of the sequence data for this patent did not format directly part of the sequence data for this patent did not format directly patent did not format directly the sequence data for this patent did not format directly patent did not format directly the sequence data for this patent did not format directly patent did not format directly the sequence data for this patent did not format directly patent did not format directly the sequence data for this patent did not format directly patent did not format directly the sequence data for this patent did not format directly patent did not format directly the sequence data for this patent did not format directly the sequence data for the sequence data for this patent did not format directly the sequence data for the sequence data for this patent did not format directly data for the sequence data for th
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genes from Drosophila and
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11-JUL-2000;
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                                                                                                   12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myoclonic epilepsy ragged red fibre syndrome; neuroprotective; nootropic; antidiabetic; anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
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                                                                                                                                                                                                                                          04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitochondrial; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human heat
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(MITO-)
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   BUCK INST AGE RES.
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2000US-00614150
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54.5%;
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ome; MERRF; cancer;
anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 805;
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                                                                                                             05-DEC-1996;
25-MAR-1997;
14-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ghosh SS,
Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, anticiabetic, antiartentricine, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
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                                                                                                                                                                                                                                                                cytoplasmic
                                                                                                                                                                                                                                                                             Vaccine; probe;
                                                                                                                                                                                                                                                                                                 H. pylori ORF 02ge41622_34176513_c1_50 outer membrane protein
                                                                                                                                                                                                                                                                                                                            08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                    AAY11027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondrial protein
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                          N-PSDB; AAX30556
                                                                                                                                                                05-DEC-1997;
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                                                                                                                                                                                                                                        Helicobacter pylori.
                                       WPI; 1998-333051/29
                                                              Smith D,
                                                                                       (ASTR ) ASTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to novel mitochondrial targets that
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                                                                                                                                                                                                                                                                                                                                                                              standard; protein; 220
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                                                               Alm
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                                                                                                                                                                                                                                                                protein;
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                                                                                        AВ.
                                                                                                              96US-00759625.
97US-00823745.
97US-00891928.
                                                                                                                                                                 97WO-US022104
                                                                                                                                                                                                                                                               diagnostic; ORF; cell envelope protein; secreted
tein; cellular protein.
                                                              Doig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%;
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Pred.
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                                                                 Castriotta
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New isolated Helicobacter pylori nucleic

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used to develop products

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ARESULT 22
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AD AAM98208
AC AAM98
AC GHPO
AC HOLAI
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Matches 7
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24-JUN-1997;
29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are disclosed, together with the nucleic acids encoding them. In all, 97 cycoplasmic proteins, secreted proteins or other cellular proteins, vaccines containing the nucleic acids or proteins are called as are probes containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection
This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                          New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INMR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 97
                                                                                                                                                                                     Claim 8; Page 111-113; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX13927.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHPO protein;
peptic ulcer (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW98208 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kleanthous H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pylori GHPO 635 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the diagnosis,
er Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MERIEUX ORAVAX PASTEUR MERIEUX SERUMS HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGLVLGGQFM 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFGVVLGGKFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease
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97US-00881227.
97US-00902615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter infection; gastroduodenal disease; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US006371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevention and treatment species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; 1
2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of infection by H. pylori and
                                                                                                                                                                                                                                                                                                                                                                                                                                  ŗ,
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                                                                                        Query Match
Best Local S
Matches 7
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Matches
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                                                                                                                                                                                                                                                 The invention relates to a vaccine for preventing or treating infections by Helicobacter pylori. The vaccine contains at least one isolated H. pylori polypeptide, or its fragments, in a carrier, where the carrier is a Salmonella, Vibrio cholerae or Shigella vector containing a nucleic acid encoding the H. pylori polypeptide. The vaccines induce humoral and cellular immune responses. The vaccines are used to treat or prevent infections by H. pylori. Sequences AAX75779 to AAX75837 represent nucleic acid sequences encoding H. pylori outer membrane polypeptides (OMPB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane polypeptide; OMP; vaccine; H. pylori infection; humoral; cellular immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 220 AA;
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                                                                                                                                                                                    Sequence 220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cellular vaccine against Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX75814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-326698/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ellis
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17-DEC-1997;
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                                                                                                                                                                                                                                     AAY17160
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70
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                                                                                        Similarity 7; Conser
                                  GAGLVLGGQFM 13
                                                                                                                                                                                                                                to AAY17218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 269-270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFGVVLGGKFV 80
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GFGVVLGGKFV
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                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00959131.
97US-00993001.
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                                                                                                               58.2%;
80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220
                                                                                        Score 39; DB
Pred. No. 2.8e
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 2;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith
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                                                                                                                                       B
                                                                                                                 .8e+02;
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                                                                                                                                       Length
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ABU22234

standard;

protein;

419

ABU22234;

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CC of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

(2) encoding a polypeptide whose expression is inhibited by the antisense

(3) an isolated

(4) an isolated

(5) encloid acid; (5) a host cell containing the vector; (3) an isolated

(6) colypeptide or its fragment whose expression is inhibited by the

(7) antisense nucleic acid; (4) an antibody capable of specifically binding

(8) contisense nucleic acid; (4) an antibody capable of specifically binding

(9) proliferation or the activity of a gene in an operon required for

(1) groliferation; (7) identifying a compound that influences the activity of

(1) identifying a gene required for cellular proliferation or the biological

(2) pathway in which a proliferation or that inhibits cellular proliferation; (8)

(8) crequired for proliferation or that inhibits proliferation of an

(8) crompound's activity; (11) a culture comprising strains in which the gene

(2) compound's activity; (11) a culture comprising strains in which the gene

(3) compound's activity; (11) a culture comprising strains in which the gene

(4) compound's activity; (11) a culture comprising strains in which the gene

(5) compound's activity; (11) a culture comprising strains in which the gene

(6) compound's activity; (11) a culture comprising strains in which the gene

(8) creating; or (13) identifying the target of a compound that inhibits the

(8) creating; or (13) identifying the target of a compound that inhibits the

(9) creating; or (13) identifying the target of a compound that inhibits the

(14) creating protains or screening for homologous nucleic acids required

(15) creating prokaryotic essential genes. Note: The sequence data for this

(16) probaryotic essential genes. Note: The sequence data for this

(17) prohypotic essential genes. Note: The sequence data for this

(18) prohypotic essential genes. Note: The sequence data for this

(18) prohypotic essential genes in the content of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #7761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-)
                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e invention relates to an isolated nucleic acid comprising any one of
e 6213 antisense sequences given in the specification where expression
the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 50158; 1766pp; English
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Forsyth
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Xu HH;
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Query Match
Best Local Similarity
Matches 8; Conserv

Conservative

58.2%;

Score 39; DB 6; Pred. No. 5.5e+02; 2; Mismatches 3

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0

Gaps

0

RESULT 26
ABR53218
ID ABR53
XX

ABR53218 standard; protein; 770 AA.

0

Length 419; Indels

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RESULT 25
ADE86082
ID ADE86
XX Clai
XX Cla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of an efflux protein thought to be involved in the biosynthesis of the peptide antibiotic AC98 of CC Streptomyces hygroscopicus NS17 (NRRL 30439). The sequence is predicted CC from an open reading frame (ORP10) in a gene cluster ADE86070 isolated CC complex. Sequence comparisons of specific ORFs indicated that the encoded CC complex. Sequence comparisons of specific ORFs indicated that the encoded CC proteins are tailoring enzymes involved in modification of the AC98 CC peptide core, e.g. glycosylation, methylation or acylation, or in CC resistance. The invention provides a method of producing NRRS using CC transformed host cells. It also provides a method of producing a cyclic CC peptide antibiotic, such as AC98, using the NRPS comprised of mppA CC lipoglycopeptide antibiotic with activity against Gram-positive CC pathogens. Also provided are methods of modifying NRPS to produce an CC antibiotic having a modified peptide core, and a method for evaluating CC antibiotic having a modified peptide core, and a method for evaluating CC the structural regions of the modified peptide.
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                                                                                                                         Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE86082 standard; protein; 450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; SEQ ID NO 30; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non-ribosomal peptide synthetase, useful for preparing antibacterial peptides, derived from Streptomyces, also related nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-812536/76.
N-PSDB; ADE86070.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2002; 2002US-0368713P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2003; 2003WO-US009746.
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                                                                                                                                                                                                                                                   Sequence
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305 FGAGGLLGGLF 315
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                                                            2 FGAGLVLGGQF 12
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                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibiotics.
                                                                                                                                                                                                                                                       450 AA;
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                                                                                                                             Conservative
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                                                                                                                                                           58.2%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenstein
                                                                                                                                                           Score 39; DB 7;
Pred. No. 5.9e+02;
                                                                                                                                Mismatches
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ADK63726
ID ADK63726
ID ADK63726
AC ADK63
AC ADK63
AC D1666
XX D1666
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                           ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 1301; 17pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae
              EP1338608-A2
                                          Unidentified
                                                                    protein
                                                                                              Disease treating protein complex-derived protein #790.
                                                                                                                         06-MAY-2004
                                                                                                                                                    ADK63726;
                                                                                                                                                                               ADK63726 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated protein complexes useful for diagnosing a disease or disease, or as a target for an active agent of a pharmaceutical,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACC61260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multiprotein complex; eukaryote; drug target; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR53218;
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                                                                                                                                                                                                                                                  142
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                                                                                                                                                                                                                                                                          2 FGAGLVLGGQ 11
                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                   complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELLZOME AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence #SEQ ID 1301.
                                                                                                                                                                                                                                                                                                                                                         770
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|FSAGLVIGGK 151
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                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to multiprotein complexes from eukaryotes.
                                                                   drug
                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grandi P,
                                                                                                                                                                                                                                                                                                                  58.2%;
70.0%;
                                                                   target; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superti-Furga GD;
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                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                  Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krause R,
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                                                                                                                                                                                                                                                                                                                 1e+03;
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                                                                                                                                                                                                                                                                                                                               Length 770;
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RESULT 28
ABJ26177
ID ABJ26
XX
ABJ26177
ID ABJ26
XX
ABPET
XX
ABPET
XX
FUNGI
KW FUNGI
KW FUNGI
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ABPET
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marzioch M, Grann-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 770 AA;
                                                                                                                                                                                                                                                                                                                                             Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABJ26177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ26177 standard; protein; 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel protein complexes comprising a first and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 1579; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder in a subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gavin A,
M, Grandi
                                                                                                                                                                                                                                                                                                                                          fumigatus essential
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i P, Krause R,
n C, Rick J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.2%;
70.0%;
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Pred. No. 1e+0
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                             gene protein #835
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use U, Merino A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1e+03;
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Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.

23-APR-2002; 2002WO-US013142

31-OCT-2002

Aspergillus fumigatus

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RESULT 29
ABJ257
ID ABJ25
XX ABJ25
XX ABJ25
XX ABJ25
XX ABDeI
C ABPeI

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Best Local
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27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-)
                                                                                                                                                               Fungicide; cytostatic;
cancer; contamination;
                                                                                                                                                                                                                                                               Aspergillus fumigatus essential gene protein #235.
                                                                                                                                                                                                                                                                                                                               16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ25577 standard; protein; 811 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 810
                                     WO200286090-A2
                                                                                                  Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to novel purified or isolated nucleic acids of ential genes of Aspergillus fumigatus. The isolated nucleic acids cinvention are used to treat or prevent infections by a pathogenic anism such as A. fumigatus, to treat a non-infectious disease in a anism such as A. fumigatus, to treat a non-infectious disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a prote gillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSAGLVIGGK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGAGLVLGGQ 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                      essential gene; Asp
biofilm; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB |
Pred. No. 1.1e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1e+03;
                                                                                                                                                                                                 Aspergillus fumigatus; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                          immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 810;
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OS Pse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc subject (e.g. cancer) to prevent or contain containation of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a C by A. fumigatus, or to prevent or inhibit formation on a surface of a C contain comprising A. fumigatus. The polynucleotides are useful for C expressing recombinant protein for characterisation, screening or C expressing recombinant protein for characterisation, screening or C corganisms invade or reside, for comparing with the DNA sequence of A. C c funigatus to identify duplicated genes or paralogues having the same or segmences of other related or distant pathogenic organisms to identify sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and C making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an C response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding c interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of the invertion
                                                                                                                                                                                                                                                                             문
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                                                                                                                                                                                                                     RESULT 30
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Best Local
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27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295890P.
09-UUL-2001; 2001US-03103899P.
31-AUG-2001; 2001US-0316362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-2002; 2002WO-US013142
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                         Pseudomonas
                                                                                                             29-JUL-2004
                                                                                                                                                                                     ABO76231 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              factors. This sequence represents a prote
of Aspergillus fumigatus of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                              811 AA;
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| FSAGLVIGGK 157
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                                                                       aeruginosa polypeptide #8406.
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                                                                                                           (first entry
                                                                                                                                                                                   protein; 903
                                                                                                                                                                                                                                                                                                                                                                          58.2%;
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                                                                                                                                                                                                                                                                                                                                                                        Score 39;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             Length 811;
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of.

Bacterial infection; Pseudomonas aeruginosa infection;

antibacterial.

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aeruginosa

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The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosis and CC therapy of pathological conditions, as molecular targets for diagnostics, CC prophylaxis and treatment of pathological conditions resulting from a CC for the ability to bind a P. aeruginosa nucleic acid, as components of CC effective antibacterial targets, as targets for antibacterial drugs, CC including anti-P. aeruginosa drugs, as templates for recombinant CC production of P. aeruginosa-derived peptides or polypeptides, as target for antibacterial drugs, CC infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-CC ABO84396 represent P. aeruginosa polypeptides of the printed CC sequence data for this patent did not form part of the printed CC sequence data for this patent did not form part of the printed CC sequence data for this patent did not form part of the printed CC sequence data for this patent did not form part of the printed CC sequence data for this patent did not form part of the printed CC sequence data.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-615305/.
N-PSDB; ABD09802.
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27-JUL-1998;
                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                         Zea mays protein fragment SEQ ID NO: 43019.
                                                                                                                                                                                                         AAG35239 standard; protein; 191
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 24977; 455pp; English
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            25-FEB-2000; 2000EP-00301439.
                                  06-SEP-2000.
                                                                         Zea mays subsp. mays.
                                                                                               termination sequence;
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98US-0094190P.
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Pred. No. 1.5e+03;
1; Mismatches 1
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  30-APR-1999;
04-MAY-1999;
05-MAY-1999;
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14-MAY-1999,
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99US-0131449P

99US-013248P

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99US-013248P

99US-013421P

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99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126785P.
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99US-0128714P.
99US-0129845P.
99US-0130077P.
99US-0130449P.
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3-0143542P. 3-0143624P. 3-0144005P. 3-0144085P.

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23-MAR-1999
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01-APR-1999;
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  99US-0121825P.
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99US-015833P.
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99US-0159331P.
99US-0159637P.
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3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathway; metabolic pathway;
expression control; promoter;
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S-0144085P S-0144325P S-0144332P S-0144333P S-0144333P S-0144333P S-0144332P S-0144332P S-0144632P S-0144632P S-0145086P S-0145086P S-0145089P S-0145089P

S-0146386P S-014738P S-0147738P S-0147738P S-0147720P S-0147192P S-0147192P S-0147192P S-0147193P S-014831P S-014831P S-014834P S-0148368P S-0149175P S-0149722P S-0149722P S-0149723P S-0149723P S-0149723P S-0149723P S-0151066P S-01511066P S-0151066P S-0151068P S-0153070P S-015303P S-0154039P S-0154039P S-0154039P S-0154039P S-0155486P S-0156458P S-0156458P

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99US-0141642P. 99US-0142154P. 99US-0142055P. 99US-0142059P. 99US-0142803P. 99US-0142977P. 99US-0143297P. 99US-0143624P. 99US-0144624P. 99US-0144625P. 99US-0144085P. 99US-0144325P. 99US-0144331P.	99US-0130077P 99US-0130449P 99US-01310449P 99US-0132467P 99US-0132467P 99US-0132468P 99US-0132468P 99US-0132468P 99US-0132468P 99US-0134256P 99US-0134256P 99US-0134256P 99US-01342719P 99US-01342719P 99US-0134271P 99US-0134271P 99US-0135124P 99US-0135124P 99US-0135124P 99US-0135124P 99US-0135124P 99US-0135129P 99US-0137222P 99US-0137222P 99US-0137222P 99US-0137222P 99US-0137222P 99US-013724P 99US-013724P 99US-0139457P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139459P 99US-0140554P 99US-0140554P	-0128234
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RESULT 33
AAG40537
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AC AAG4(
XXX Pro
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XX Arah
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28-OCT-1999
29-OCT-1999
25-FEB-1999;

05-MAR-1999;

09-MAR-1999;

23-MAR-1999;

25-MAR-1999;

25-MAR-1999;

01-APR-1999;

06-APR-1999;

16-APR-1999;

16-APR-1999;

19-APR-1999;

23-APR-1999;

23-APR-1999;
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hybridisation assay; genetic mapping; gene expression control; promoter;
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Similarity 66.7%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
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99US-0159239P

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99US-0121825P
99US-0123180P
99US-012548P
99US-0125788P
99US-0126264P
99US-0126785P
99US-0127462P
99US-0128234P
99US-01282714P
99US-0129845P
99US-0130610P
99US-0130891P
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Pred. No. 3.5e+02;
2; Mismatches 1;
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21-UN-1999
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           99US-0131449P.
99US-0132484P.
99US-0132484P.
99US-0132487P.
99US-0132487P.
99US-0132487P.
99US-0134218P.
99US-013421P.
99US-013421P.
99US-0134221P.
99US-0134221P.
99US-0134221P.
99US-013422P.
99US-013622P.
99US-013945P.
99US-01492P.
99US-01492P.
99US-01492P.
99US-014425P.
99US-0144342P.
99US-0144331P.
99US-0144333P.
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RESULT 34
AAG04531
ID AAG044531
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AC AAG04
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KW Prot
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hybridisation assay; genetic mapping; gene expression control; promoter;
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   APR-1999
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-MAR-1999;
-MAR-1999;
-MAR-1999;
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Similarity 66.7%;
6; Conservative
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99US-0160981P.
99US-0160981P.
99US-01614098P.
99US-0161405P.
99US-0161361P.
99US-0161361P.
99US-0161361P.
99US-0161993P.
99US-0161993P.
99US-0161993P.
   99US-0121825P.
99US-012348P.
99US-0125788P.
99US-01267864P.
99US-0127462P.
99US-0127462P.
99US-0128234P.
99US-0130077P.
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Pred. No. 3.7e
2; Mismatches
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3.7e+02;
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S-0144014P.
S-0145086P.
S-0145089P.
S-0145089P.
S-0145214P.
S-0145214P.
S-0145218P.
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S-0145219P.
S-0147204P.
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S-01471302P.
S-01471302P.
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S-014713P.

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99US-0144331P. 99US-0144332P. 99US-0144333P. 99US-0144335P. 99US-0144352P. 99US-0144632P. 99US-0144814P. 99US-0145086P. 99US-0145086P. 99US-0145087P. 99US-0145089P. 99US-0145089P. 99US-0145089P.	99US-0134218P 99US-0134218P 99US-0134718P 99US-0134778P 99US-0135124P 99US-0135124P 99US-0135021P 99US-0136721P 99US-0136722P 99US-0136722P 99US-0137528P 99US-0137528P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-014952P 99US-0142803P 99US-0142803P 99US-0142803P 99US-0142803P 99US-0142803P 99US-0142803P 99US-0142803P 99US-0142803P 99US-0142803P 99US-0142803P 99US-0142803P 99US-014364P 99US-014364P 99US-014364P 99US-014364P	99US-0132863P. 99US-0134256P.
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RESULT
ADGA 531
ADGA 6531

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Matches 6
25 FEB-1999
05 -WAR-1999
09 -WAR-1999
23 -WAR-1999
25 -WAR-1999
06 -APR-1999
06 -APR-1999
16 -APR-1999
17 -APR-1999
21 -APR-1999
21 -APR-1999
23 -APR-1999
23 -APR-1999
23 -APR-1999
24 -WAY-1999
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nilarity 66.7%;
Conservative ;
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99US-0121825P

99US-0123548P

99US-0125788P

99US-0126785P

99US-0127462P

99US-0128714P

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99US-0130047P

99US-01300449P

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99US-0160981P.
99US-0161404P.
99US-0161406P.
99US-0161360P.
99US-0161359P.
99US-0161361P.
99US-0161361P.
99US-0161361P.
99US-0161932P.
99US-0161993P.
99US-0161993P.
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Pred. No. 3.7e+02;
2; Mismatches 1
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21-MAY 1999
22-MAY 1999
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23-MAY 1999
24-MAY 1999
26-MAY 1999
27-MAY 1999
28-MAY 1999
28-MAY
99US-0134941P

99US-0135124P

99US-0135353P

99US-0135353P

99US-0136782P

99US-0137528P

99US-0137528P

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99US-014233P

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99US-0145086P

99US-0145185P

99US-0145185P

99US-0145224P

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99US-01452185P

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99US-0145918P
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-AUG-1999 -AUG-1999

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RESULT 36
AAAG04530
AAG044530
XX AAG04
XX AAG04
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XX AAG04
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PR 25-FI
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Best Local S
Matches 6
  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-APR-1999;
16-APR-1999;
16-APR-1999;
21-APR-1999;
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23-APR-1999;
23-APR-1999;
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23-APR-1999;
23-APR-1999;
24-APR-1999;
25-MAY-1999;
06-MAY-1999;
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01-MAY-1999;
11-MAY-1999;
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26-OCT-199;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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Similarity 66.7%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
99US-0121825P.
99US-0123480P.
99US-012548BP.
99US-0126785P.
99US-0126785P.
99US-0126785P.
99US-0127462P.
99US-01208714P.
99US-0130510P.
99US-0130510P.
99US-0130510P.
99US-0130510P.
99US-0132484P.
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99US-013421P.
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99US-0134535P.
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99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
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4.6e+02;
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on control;
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promoter;
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28.JUL-1999
02.AUG-1999
03.AUG-1999
04.AUG-1999
04.AUG-1999
05.AUG-1999
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99US-0145951P 99US-0146386P 99US-0146386P 99US-0147038P 99US-0147038P 99US-014720P 99US-0147192P 99US-0147192P 99US-0147192P 99US-0147416P 99US-0147492P 99US-0148171P 99US-014814P 99US-0148168P 99US-0149722P 99US-0149426P 99US-0149426P 99US-0149722P 99US-0149426P 99US-0149723P 99US-0149723P 99US-0150566P 99US-0151066P 99US-01511066P 99US-0151106P 99US-0155486P 99US-0155486P 99US-0155486P 99US-0155488P 99US-015548P 99US-0155488P 99US-0155488P 99US-0155488P 99US-0155488P 99US-0155488P 99US-0155488P 99US-015933P 99US-015933P 99US-015933P 99US-015933P 99US-015933P 99US-015933P 99US-016076P 99US-016076P 99US-0160815P 99US-0160815P 99US-0160881P 99US-0160980P 99US-0161406P 99US-0161406P 99US-0161406P

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	99US-0147302P.	9US-0	9US-0	9US-0	9US-0	908-0	908-0	900			0-2116	9119	0-506	9US-0	908-0	908-0	0-0	0110	9US-0	9US-0	9US-0	9US-0	9US-0	9US-0	0-S06	905-0	905-0	905-0		0110	0-506	0-5116	9US-0	9US-0	9US-0	0-506	0-506	0-0		0-2116	9US-0	905-0	9US-0	9US-0	908-0	0-806	908-0	908-0	908-0	908-0	908-0	905-0	908-0	0-00	908-0	908-0	0-506	9US-0	908-0	908-0	9US-0	905-0	905-0	200	0	0.00	0-0				9115-0	0110	0-5116	0-506	9US-0	0-Su6	9US-0	9US-0	
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		10-SU6	10-SN6	10-Sn6	9US-01	T0-506	TO-506	1000	100	0110-01	9115-01	905-01	905-01	10-SD6	10-506	T0-806	TO-07	9115-01	9US-01	9US-01	9US-01	10-Sn6	9US-01	10-Sn6	T0-S06	TO-SOF	10-506	10-506	10.01	0116-01	915-01	9115-01	9US-01	10-SU6	9US-01	T0-506	10-00	200-01	0110 01	0118-01	9US-01	9US-01	9US-01	10-SD6	T0-506	10-506	TO-506	TO-506	TO-506	TO-506	TO-506	10-506	TO-506	TO-506	10-506	TO-506	TO-506	10-806	10-506	10-506	10-506	TO-506	10-506	TO-506	200-01	10000	10-01	000	0110-01	0112-01	9115-01	9118-01	9115-01	905-01	9US-01	9US-01	9US-01	99US-0147192P.	

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Best Local Similarity
Matches 6; Conserv
25-FEB-1999

05-MAR-1999;

09-WAR-1999;

23-MAR-1999;

23-MAR-1999;

25-MAR-1999;

01-APR-1999;

01-APR-1999;

16-APR-1999;

16-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

24-MAY-1999;

14-MAY-1999;

15-MAY-1999;

21-MAY-1999;

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2; Mismatches 1
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Drosophila; dev pharmaceutical.
                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 22848.
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genes from Drosophila and
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                           developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 22848; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                           ADN73077 standard; protein; 249 AA.
                                                                                                                                                                       plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                                                                                                                                                                                              Thale
                                                                                                                                                                                                                                                        15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                   ADN73077;
                                                                                                                       WO2004035798-A2
                                                                                                                                               Arabidopsis thaliana.
                                                                                             29-APR-2004
                                      18-OCT-2002; 2002EP-00079408.
                                                                   20-OCT-2003;
              (CROP-) CROPDESIGN NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                            protein upregulated in E2Fa/Dpa expressing plants SeqID
                                                                    2003WO-EP011658
                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.7%;
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Pred. No. 4.6e+02;
2; Mismatches 1
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Search completed: December Job time: 9.05036 secs

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2004, 09:16:30

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FGCGVILGG

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                                                                                     Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                               the altered plant characteristics are selected from increased yield or physiology, altered endoreduplication, biochemistry, signal or physiology, altered endoreduplication, biochemistry, signal or physiology, altered endoreduplication, biochemistry, signal or physiology, storage lipid mobilisation and/or altered photosynthesis, transduction, storage lipid mobilisation and/or altered photosynthesis, transduction, storage lipid mobilisation and/or altered photosynthesis, transduction, storage lipid mobilisation and/or altered photosynthesis, transduction of cells or tissues. The identified genes play a during transformation of cells or tissues. The identified genes play a during transformation of cells or tissues. The identified genes play a wall biosynthesis, nitrogen and/ or carbon metabolism or they function as wall biosynthesis, nitrogen and/ or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale crees protein transcription factors, given in an exemplification of the invertice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up compared to the characteristics of the plants overexpressing the heterodimeric expansion of the product of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes alter plant characteristics accordingly. The product of growth regulators, generating transgenic plants for the production of growth regulators, thereas the products of the product of the product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inze
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 972; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              more proteins.
                                                                                                                                                                                                                                              Sequence 249 AA;
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                                                                                     l Similarity
6; Conserv
                 2 FGAGLVLGG 10
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                                                                                                 Conservative
                                                                                                                                            56.7%;
66.7%;
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                                                                                                          2.
                                                                                                          Score 38; DB 8;
Pred. No. 4.6e+02
2; Mismatches
                                                                                                                                                                                           Length 249
                                                                                                                       Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 2000000000
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67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1585576 segs, 357178320 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
                      /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US09S_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOME.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                              _6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                        6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                  6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Regult No.	Score	Query Match	Query Match Length DB	BB	ID	Description
1	45	67.2	123	17	US-10-425-115-267639	Sequence 267639,
N	41	61.2	97	15	US-10-424-599-197757	Sequence 197757,
ω	41	61.2	291	15	US-10-041-018-27	Sequence 27, Appl
4	41	61.2	319	14	US-10-156-761-9015	Sequence 9015, Ap
ហ	40	59.7	875	16	US-10-408-765A-1566	Sequence 1566, Ap
6	39	58.2	178	15	US-10-335-977-5090	Sequence 5090, Ap
7	39	58.2	220	9	US-09-881-752A-16	Sequence 16, Appl
œ	39	58.2	220	15	US-10-335-977-5091	Sequence 5091, Ap
9	39	58.2	403	15	US-10-425-114-48433	Sequence 48433, A
10	39	58.2	405	15	US-10-425-114-41675	Sequence 41675, A
11	39	58.2	405	15	US-10-425-114-48462	Sequence 48462, A
12	39	58.2	405	15	US-10-425-114-49554	Sequence 49554, A
13	39	58.2	419	15	US-10-282-122A-50158	Sequence 50158, A

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	1.4
38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	39	39	39	39	39	39	2.5
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327	287	7	272	270	259	257	256	249	249	249	249	249	249	249	249	249	249	241	238	182	146	102	94	94	811	810	770	748	545	528	ů,
16	17	16	17	15	15	16	15	17	17	17	17	17	17	17	17	16	15	15	16	17	14	17	17	15	14	14	14	14	14	14	1
-10-437-963-15436	0-425-115-207	-10-437-963-14082	-10-425-115-28315	-10-425-114-604	-10-425-114-4157	-10-437-963-174	0-424-599-205	-10-739-930-793	25-115-28403	-10-425-115-2831	-10-425-115-28316	-10-425-115-2831	-10-425-115-28316	-10-425-115-23196	-10-425-115-23196	37-963-17	-10-424-599-20550	-10-425-114-465	37-963-20375	-10-425-115-227	-10-369-493-222	-10-425-115-294	-10-425-115-365	-10-424-599-23165	-10-128-714-3	-10-128-714-823	-10-369-493-221	-10-369-493-324	-10-156-761-1145	-10-369-493-217	- TO-40-20-01-
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# ALIGNMENTS

RESULT 1
US-10-425-115-267639
; Sequence 267639, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

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RESULT 2
US-10-424-599-197757
; Sequence 197757, Application US/10424599
; Publication No. US20040031072A1
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                                                                                                                                                                                                                                                                  ; FEATURE: ; OTHER INFORMATION: Clone ID: MRT4577_175692C.1.pep US-10-425-115-267639
                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 267639
LENGTH: 123
TYPE: PRT
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays
                                                                                                                                                                                Local Similarity 63.6%; les 7; Conservative
                                                                                                                    36
                                                                                                                  1 EFGAGLVLGGQ 11
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36 DYGSGLVIGGQ 46
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Pred. No. 14;
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                                                                                                                                                                                            Indels
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                                                                                                                                                                                            Gaps
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PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SOPTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 291
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-10-041-018-27
                                                         GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH;
APPLICANT: SKIBA, TADAYOSH;
APPLICANT: HATTORI, MASAHI
                                                                                                                                                                                                                                 US-10-156-761-9015
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CURRENT APPLICATION NUMBER: US/10/424,599
UNDER OF SEQ ID NOS: 285684
SEQ ID NO 197757
LENGTH: 97
TYPE: ppr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                        Sequence 9015, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_205C.1.pep
US-10-424-599-197757
                         APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIHA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Applicat Publication No. US200 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT APPLICATION NUMBER: 05/10/041,018
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ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 63.6%; es 7; Conservation
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les 8; Conserv
                                                                                                                                                                                                                                                                                              153 FGVGGILGGQY 163
APPLICATION NUMBER: US/10/156,761
                                                                                                                                                                                                                                                                                                                               2 FGAGLVLGGOF 12
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                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 15; Length 291; Pred. No. 1.5e+02;
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RESULT 6
US-10-335-977-5090
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Fahy, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
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                                                                                                                                              Sequence 5090, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
CHAPTING TO HELICOBACTER PYLORI FOR
DIGAMOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WATNOCK, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660084 465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 1566
LENGTH: 875
TYPE: B75
TYPE: B77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9015
LENGTH: 319
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Best Local Similarity
Watches 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-9015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-408-765A-1566
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.7%; Score 40; DB 16; Length 875; Best Local Similarity 54.5%; Pred. No. 6.5e+02; Matches 6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1566, publication No.
ZIP: 02109-1875
COMPUTER READABLE FORM:
                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                        169 DFSAGLIIGGK 179
                                                                                                                                                                                                                                                                                                                                                                                       1 EFGAGLVLGGQ 11
                                  STREET: 28 State Stre
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 GGGLVLGGQ 151
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ion No. US20040101874A1
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                                                                                 28 State Street
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 319;
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APPLICANT: Kleanthous, Harold
APPLICANT: Kleanthous, Amal
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome
FILE APPLICATION: Genome
FILE OF INVENTION: Genome
FILE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: F8stSEQ for Windows Version 4.0
SEQ ID NO 16
SEQ ID NO 16
SEQ ID NO 179E: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...178
SEQUENCE DESCRIPTION: SEQ ID NO: 5090:
US-10-335-977-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-881-752A-16
; Sequence 16, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
                                                                                                                                                    US-09-881-752A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 5090:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acids
                                                               Query Match 58.2%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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1es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
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3 GAGLVLGGQFM 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 15; Length 178; Pred. No. 1.8e+02;
                                                               Score 39; DB 9;
Pred. No. 2.3e+02;
3; Mismatches 1
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                                                                 1; Indels
                                                                                                         Length 220;
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      APPLICANT
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NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...220
SEQUENCE DESCRIPTION: SEQ ID NO: 5091:
US-10-335-977-5091
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Best Local Similarity
Thehes 7; Conserve
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Sequence 48433, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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US-10-335-977-5091
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Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

                                                                                                                                              APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5091:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 GEGVVLGGKEV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 GFGVVLGGKFV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GAGLVLGGQFM 13
| |:||||:|:
Zhou, Yinua
Kovalic, David K
Screen, Steven I
Tabaska, Jack E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 220 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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63.6%;
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Pred. No. 2.3e+02;
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US-10-425-114-41675
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US-10-425-114-41675
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                                                                                                                                                                                                  Sequence 48462, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: LIB3068-059-A10_FLI.pep
US-10-425-114-48433
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313))B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 41675
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 48433

LENGTH: 403

THE TITLE OF INVENTION INCLEDED ASSOCIATION OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41675, Application US/10425114
Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
RUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 15;
Pred. No. 4.3e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 405;
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APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Kovalio, David K. APPLICANT: Kovalio, David K. APPLICANT: Kovalio, David K. APPLICANT: Tabaska, Jack E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILIR EFERENCE: 38-21(5313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NO49554 LENGTH: 405
                                                                                                                                                                                                                                                  US-10-282-122A-50158
; Sequence 50158, Application US/10282122A
; Publication No. US20040029129A1
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; OTHER INFORMATION: Clone ID: LIB3689-213-B12_FLI.pep
US-10-425-114-49554
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Best Local Similarity
"arches 7; Conserve
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Best Local S
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                                                                                                         APPLICANT:
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APPLICANT:
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carl
APPLICANT: Malone, Chery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 48462
LENGTH: 405
                                               TITLE OF INVENTION: Identification of Essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
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                                                                         Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                           EFGAGLVLGGQFM 13
                                                                                                                                                                  Haselbeck, Robert
Ohlsen, Kari
                                                                                                                       Trawick, John
                                                                                                                                        Wall,
                                                                                                                                                    Zyskind, Judith
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                                                                                                                                                                                                                                                                                                                                                                                                                    58.2%;
53.8%;
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Pred. No. 4.3e+02;
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Pred. No.
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RESULT 15
US-10-369-493-21791
; Sequence 21791, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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US-10-402-842-30
(S-quence 30, Application US/10402842
Publication No. US20030219872A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                            Query Match
Best Local Similarity
Tarches 8; Conservi
                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptomyces hygroscopicus US-10-402-842-30
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                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Magarvey, Nathan A.
APPLICANT: Hucul, John A.
APPLICANT: Hucul, John A.
TITLE OF INVENTION: NON-RIBOSOMAL PEPTIDE SYNTHETASES AND ASSOCIATED BIOSYNTHETIC GEN
FILE REFERENCE: 0630/1J854-US1
CURRENT APPLICATION NUMBER: US/10/402,842
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/368,713
PRIOR FILING DATE: 2002-03-30
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 30
LENGTH: 450
TYPE: PRT
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50158
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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Pred. No. 4.4e+02;
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US-10-369-493-3245
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION UMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
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US-10-156-761-11459
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                        RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11459, Application US/10156761
Publication No. US20030119018A1
GEMERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21791
LENGTH: 528
TYPE: PRT
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LENGTH: 545
TYPE: PRT
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Best Local
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 388-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                               332 AGLILGGLFL 341
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                                                                                                         4 AGLVLGGQFM 13
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Pred. No. 5.8e
2; Mismatches
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Pred. No.
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Sequence 3245, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.

APPLICANT:

Hinkle, Gregory J. Slater, Steven C. Goldman, Barry S.

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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-8
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22168
LENGTH: 770
TYPE: PRT
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US-10-369-493-22168
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3245
LENGTH.
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US-10-128-714-8235
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Best Local S
Matches 7
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Best Local Similarity
Matches 7; Conserv
Sequence 8235, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Emwidio, Carlos
APPLICANT: Exoshkin, Alexey M
APPLICANT: Lemieux, Sebbastien M
APPLICANT: Lemieux, Sebbastien M
APPLICANT: Lemieux, Sebbastien M
APPLICANT: Lemieux, Sebbastien M
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
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APPLICANT: Hinh
APPLICANT: Slat
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NAME/KEY: unsure
LOCATION: (1)..(748)
OTHER INFORMATION: unsure at all Xaa locations
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TYPE: PRT
ORGANISM: Neurospora crassa
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70.0%;
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70.0%;
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Pred. No.
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Pred. No. 8e+02;
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         and
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APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Longerous, Sebastien M
APPLICANT: NUMER: US/10/128,714
CURRENT APPLICATION NUMBER: US/60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
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FILE REFERENCE: 10182-018-999
CURRENT FILING DATE: 2002-04-23
PRIOR REPLICATION NUMBER: US 60/285,697
PRIOR PELING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
SEQ ID NO 8235
LENGTH: 810
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US-10-128-714-3235
닭
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3235, Application US/10128714 Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SEQ ID NO 3235
LENCTH: 811
TYPE: PRT
                                                                                                              Query Match
Best Local
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  148 FSÁGLVIGGK 157
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                                                                                      Similarity 7; Conserv
                                            FGAGLVLGGQ 11
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Pred. No.
                                                                                           2; Mismatches
                                                                                                                  Score 39; DB 14;
Pred. No. 8.7e+02;
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RESULT 23
US-10-425-115-294011
; Sequence 294011, Application US/10425115
; Publication No. US20040214272A1
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Best Local Similarity
Thes 6; Conserve
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 365962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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SEQ ID NO 231652
LENGTH: 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 365962, Application US/10425115 Publication No. US20040214272A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT PPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
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APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                        LENGTH: 94
TYPE: PRT
ORGANISM: Zea mays
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NAME/KEY: unsure
LOCATION: (1)...(94)
OTHER INFORMATION: unsure at all Xaa locations
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Pred. No. 1.4e
2; Mismatches
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Pred. No. 1.4e+02;
4; Mismatches 1
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1.4e+02;
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Query Match
Best Local Similarity
Thes 7; Conserve
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NAME/KEY: unsure
; LOCATION: (1)..(146)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2228
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US-10-369-493-2228
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US-10-425-115-294011
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SEQ ID NO 2228
LENGTH: 146
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SEQ ID NO 294011
LENGTH: 102
                                                                 Matches
                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EXPRESSION OF MICROBIAL TITLE OF INVENTION: PLANTS WITH IMPROVED PIFILE REFERENCE: 38-10(52052)B
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                ORGANISM: Schizosaccharomyces pombe
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                                                              Similarity
6; Conserve
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                                2 FGAGLVLGGQ 11
FGTGIILAGQ
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                                                                                 56.7%;
                                                                                 Score 38;
Pred. No.
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Pred. No.
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1.5e+02;
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US-10-425-115-227826, Application US/10425115; Sequence 227826, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua

RESULT 25

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; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139373C.1.pep
US-10-425-115-227826
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 227826
LENGTH: 182
                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_98906C.1.pep
US-10-437-963-203753
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US-10-425-114-46558
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Best Local
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 203753
LENGTH: 238
LENGTH: 238
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TYPE: PRT
ORGANISM: Zea mays
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APPLICANT:
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
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                              APPLICANT:
APPLICANT:
APPLICANT:
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                                             APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
CANT: Cao, Yongwei
OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
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Cao, Yongwei
Wu, Wei
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70.0%;
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Pred. No. 2.7e+02;
1; Mismatches 2
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Pred. No. 3.6e+02;
1; Mismatches 2;
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: FILE REFERENCE: 38-21(53313)B
:CURRENT APPLICATION NUMBER: US/10/425,114
:CURRENT FILING DATE: 2003-04-28
:NUMBER OF SEQ ID NOS: 73128
:SEQ ID NO 46558
:SEQ ID NO 46558
:TYPE: PRT
:CORGANISM: Zea mays
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US-10-425-114-46558
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FULE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205502
LENGTH: 249
TYPUE: OPP
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US-10-437-963-174772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53221)B
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                              Sequence 174772, Application US Publication No. US20040123343A1
                                                                                                                                                                                                                                                                             GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                      APPLICANT:
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les 6; Conserv
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Similarity 66.7%;
6; Conservative
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                                                                                                                                                 Boukharov, Andrey
Barbazuk, Brad
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                                                                                                                                                                                                        Yongwei
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Pred. No. 3.7e
2; Mismatches
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pred. No. 3.8e+02;
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 231963
LENGTH: 249
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 231962
LENGTH: 249
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                                                                                                                                                                                                                                                                                                                                                                                                             US-10-425-115-231963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: US-10-425-115-231962
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                                                      ); OTHER INFORMATION: US-10-425-115-231963
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Best Local Similarity
Query Match
Best Local Similarity
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ORGANISM: Zea mays
                                                                                         FEATURE:
                                                                                                          ORGANISM: Zea mays
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ORGANISM: Oryza sativa
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                                                                     Clone ID:
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56.7%;
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Pred. No.
Score 38; DB 17;
Pred. No. 3.8e+02;
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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US-10-425-115-283165
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US-10-425-115-283162
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283162
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Best Local S
Matches 6
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SEQ ID NO 283165
LENGTH: 249
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                      TYPE: PRT
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132 FGCGVILGG 140
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Pred. No. 3.8e
2; Mismatches
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                                                                                  Score 38; DB 17;
Pred. No. 3.8e+02;
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                                                                                                  DB 17; Length 249;
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RESULT 34 US-10-425-115-283167

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APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322))B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283173
LENGTH: 249
RESULT 36
US-10-425-115-284033
; Sequence 284033, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
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US-10-425-115-283173
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283167
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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Publication No. US20040214272A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(249)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                 Local Similarity 66.
nes 6; Conservative
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ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                    56.7%;
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Pred. No.
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Page 10

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 284033

LENGTH: 249

TYPE: TO
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; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C3166_22.p
US-10-739-930-7930
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US-10-424-599-205503
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                           Sequence 20503, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La ROSa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285884
SEQ ID NO 205503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 7930
LENGTH: 249
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53377) B
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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ORGANISM: Zea mays
FEATURE:
                 LENGTH: 256
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6; Conserv
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66.7%;
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Pred. No.
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Pred. No.
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ORGANISM: Glycine

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEO ID NOS: 204966
SEO ID NO 174771
LENGTH: 257
TYPE: PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
""" hes 6; Conserve
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Sequence 41579, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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; ORGANISM: Oryza sativa
; PEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72681C.1.pep
US-10-437-963-174771
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_27598C.1.pep
US-10-424-599-205503
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APPLICANT: Lii, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 41579
LENGTH: 259
TYPDE: DET
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Best Local Similarity 66.7%;
Matches 6; Conservative
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NAME/KEY: unsure
LOCATION: (1)..(256)
OTHER INFORMATION: unsure at all Xaa locations
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llarity 66.7%;
Conservative
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Pred. No. 3.9e+02;
2; Mismatches 1
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; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3078-037-G4_FLI.pep
US-10-425-114-41579
Search completed: December Job time : 5.58273 secs
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                                                                                                       Query Match
Best Local Similarity 66.
Matches 6; Conservative
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                                                      142 FGCGVILGG 150
                                                                               2 FGAGLVLGG 10
                                                                                                                      56.7%;
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Pred. No. 3
                                                                                                          Mismatches
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                            1910
1823.5
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seq length: 2000000000
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Match
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/US08_EW_PUB.pep:*
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cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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cgn2_6/ptodata/2/pubpaa/PCT_NEW_
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                        9 US-09-313-942-8

9 US-09-935-868-8

14 US-10-287-035-8

14 US-10-282-162-8

14 US-10-247-463-12

15 US-09-313-942-15

16 US-09-935-868-15

17 US-09-935-868-15

18 US-09-935-868-26

18 US-09-313-942-26

18 US-09-313-942-26
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Sequence 8, Appli
Sequence 8, Appli
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Sequence 12, Appli
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 14, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
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.4. 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
927	930	930.5	930.5	934	934	w	936.5			•					938.5							954.5	1683	1683	1683	1683	1783	1783	1783	1783	1788
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183	207	212	212	186	184	317	347	212	212	212	212	212	212	212	212	212	212	212	212	212	460	387	315	315	315	315	1168	1168	1168		1158
16	15	17	9	14	14	14	17	17	17	17	17	16	16	15	14	14	14	14	9	φ	14	16	14	14	9	9	14	14	9	9	14
-10-658		-10-197	US-09-908-594-14	-10-083-	-10-053-	US-10-083-446-145	-10-763-	-10-276	-10-866-540-	-10-828-343-	US-10-773-654-13	Ļ		-10-440-464-	1			US-10-099-007A-3	09-854-	US-09-854-280-14	US-10-247-463-13	-10-3	•	US-10-287-035-16	935-	US-09-313-942-16		US-10-287-035-24	935-868-	US-09-313-942-24	US-10-282-162-26
198, 7	e 3061	e 14	L	163	Sequence 3, Appli	14!	8,	φ,	13		e 13	13	13	61,	e 13,	e 13,	e 13,	e u	14,	Sequence 14, Appl	13	14	16,	e 16,	16,	`	24,	e 24,	24, F	24, I	Sequence 26, Appl

## ALIGNMENTS

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; SOFTWARE: FASTSEQ for Win

; SEQ ID NO 8

; LENGTH: 592

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-313-942-8
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CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20020012962x1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
121 CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
                                                                                                                                                                                                                             377;
                                                                         61 VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEEPQLS 120
                                               61 VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                               1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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FILE REFERENCE: REG 203D
FILE REFERENCE: REG 203D
FILE REFERENCE: REG 203D
FILE REFERENCE: REG 203D
FUNDER: 2002-04-11
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 8
SEQ ID NO 8
LENGTH: 592
TYPE: PRI
ORGANISM: Homo sapiens
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Matches 377
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                                                                                                   PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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  GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                              PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDNWSGLRHVVQLRAQEEFGQ
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APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: 05/313,942
PRIOR PILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
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PRIOR APPLICATION NUMBER: 09/313,942
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Publication No. US20030104567A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030143697A1

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

APPLICANT: REGENERON PHARMACEUTICALS, INC.

APPLICATION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING TITLE OF INVENTION: AND USING FILE REFERENCE: REG 203-B-US

CURRENT APPLICATION NUMBER: US/10/282,162

CURRENT FILING DATE: 2002-10-28

PRIOR FILING DATE: 1999-09-22

PRIOR PELING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-22
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 377;
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ORGANISM: Homo sapiens
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   AVQMSTKVL 481
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                                         PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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77.1%;
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; Pred. No. 3.7e-140;
22; Mismatches 44;
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RESULT 6
US-09-313-942-15
Sequence 15, Application US/09313942
Publication No. US20020012962A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONIS
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
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; TYPE: PRT
; ORGANISM: primate
US-10-247-463-12
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APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Memmalian Receptor Proteins; Related Reagents and
TITLE OF INVENTION: Methods
FILE REFERENCE: DX0992Q
CURRENT APPLICATION NUMBER: US/10/247,463
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US/09/588,113
PRIOR APPLICATION NUMBER: US/09/588,113
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO: 13
SOFTWARE: Patentin Ver: 2.0
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Best Local Similarity
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Pred. No. 4.6e-140;
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US-09-35-868-15
; Sequence 15, Application US/09935868
; Patent No. US20020164690A1
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PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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                  VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                               MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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Conservative (
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Pred. No. 1.3e-139;
2; Mismatches 0;
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Pred. No. 1.3e-139;
2; Mismatches 0;
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Sequence 15, Application US/10287035
Sequence 15, Application US/10287035
Publication No. US20030104567A1

GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
ITITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203DA
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 60
SOPTWARE: FastSEQ for Windows Version 3.0
TYPE: PRT
TYPE: PRT
TYPE: PRT
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US-10-287-035-15
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Local Similarity 99.4%;
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                                                                                                                                                                                                                                                                                                                        VLRKPAAGSHPSRWAGWGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS 120
GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ 357
                     GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTINKDDDNILFRDSANATSLPVE 357
                                                                                                                                               PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240
                                                                                                                                                                    PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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                                                                      PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                            PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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Pred. No. 1.3e-139;
2; Mismatches 0;
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RESULT 10
US-10-322-696-144
US-10-322-696-144, Applica
; Sequence 144, Applica
; Publication No. US200
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 56
SOPTWARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 360
TYPE: PRT
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US-10-282-162-15

Sequence 15, Application US/10282162

Publication No. US20030143697A1

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS,

TITLE OF INVENTION: AND USING
; ORGANISM: Homo sapiens
US-10-322-696-144
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                                   NUMBER OF SEQ ID NOS: 186
SOFTWARE: FRSUSEQ for Windows Version 4.0
SEQ ID NO 144
LENGTH: 453
TYPE: PRT
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Best Local Similarity
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                                                                                                                                       APPLICANT: MOTTIS, David W.
APPLICANT: Malandro, Marc
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 529452001200
CURRENT APPLICATION NUMBER: US/10/322,696
CURRENT FILING DATE: 203-10-17
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o. US20040166490A1
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Pred. No. 1.3e-139;
2; Mismatches 0;
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Sequence 26, Application US/09313942

Publication No. US20020012962A1

GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25

NUMBER OF SCT IN NCS. 12
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US-09-313-942-26
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SOFTWARE: FRStSEQ for Windows Version
SEQ ID NO 26
LENGTH: 1158
                                                                                                                                                                                                                                                     Query Match 62.9
Best Local Similarity 99.1
Matches 331; Conservative
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                                                            121 CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240
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92.5%;
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                                                                                                                                                                                                                                                       Score 1788; DB 9;
Pred. No. 2e-129;
2; Mismatches 1;
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RESULT 13
US-10-287-035-26
(US-10-287-035-26)
(Sequence 26, Application US/10287035)
(Publication No. US20030104567A1)
(GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
(TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AN
(TITLE OF INVENTION: AND USING
(FILE REFERENCE: REG 203DA
(CURRENT APPLICATION NUMBER: US/10/287,035)
(CURRENT FILING DATE: 2002-11-01
(FRIOR APPLICATION NUMBER: USSN 09/935,868)
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US-09-935-868-26
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APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists,
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
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LENGTH: 1158
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ORGANISM: Homo sapiens
-09-935-868-26
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PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
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99.1%;
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Pred. No. 2e-129;
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US-10-282-162-26

ORGANISM: Homo sapiens

TYPE: PRT LENGTH: 1158

SEQ ID NO 26

NUMBER OF SEQ ID NOS: 56 SOFTWARE: FastSEQ for Windows Version

Best Local Similarity Matches 331; Conserv

62.5%; nilarity 99.1%; Conservative

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Mismatches

Score 1788; DB 14; Pred. No. 2e-129;

Length 1158; Indels

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Gaps

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Query Match

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PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 1158
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-282-162-26
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Sequence 26, Application US/10282162
Sequence 26, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILLE REFERENCE: REG 203-B-US
FILLE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 1990-09-22
PRIOR APPLICATION NUMBER: 907/87,835
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
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Best Local Similarity
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Pred. No. 2e-129;
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 1168
TYPE: PRT
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US-09-313-942-24
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Local Similarity 99.7%;
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Pred. No. 4.9e-129;
1; Mismatches 0;
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US-10-287-035-24
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                                                      CURRENT APPLICATION NUMBER: US/10/287,035
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USXN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USXN 09/787,835
PRIOR APPLICATION NUMBER: USXN 09/787,835
PRIOR APPLICATION NUMBER: USXN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
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Patent No. US20020164690A1
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
CURRENT FILING DATE: 2002-04-11
                                                                                                                                                                                                                                   Sequence 24, Application US/10287035
Publication No. US20030104567A1
GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203DA
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 1168
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Best Local Similarity
Matches 330; Conserv
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ORGANISM: Homo sapiens
                    APPLICATION NUMBER: 09/313,942 FILING DATE: 1999-05-19
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Pred. No. 4.9e-129;
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Sequence 24, Application US/10282162

| Sequence 24, Application US/10282162
| Publication No. US20030143697A1
| GENERAL INFORMATION:
| GENERAL INFORMATION: PHARMACEUTICALS, INC.
| APPLICANT: REGENERON PHARMACEUTICALS, INC.
| TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND TITLE OF INVENTION: AND USING PILTE REFERENCE: REG 203-B-US
| CURRENT SPELICATION NUMBER: US/10/282,162
| CURRENT FILING DATE: 2002-10-28
| CURRENT FILING DATE: 2002-10-28
| PRIOR APPLICATION NUMBER: 09/787,835
| PRIOR APPLICATION NUMBER: PCT/US99/22045
| PRIOR FILING DATE: 1999-09-22
| NUMBER OF SEQ ID NOS: 56
| SOFTWARE: FRASTSEQ for Windows Version 3.0
| SEQ ID NO 24
| LENGTH: 1168
| TYPE: DET
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NUMBER OF SEQ ID NOS: 60
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 24
LENGTH: 1168
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ORGANISM: Homo sapiens
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Matches 330; Conserv
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ORGANISM: Homo sapiens
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Q ID NOS: 60
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Pred. No. 4.9e-129;
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Pred. No. 4.9e-129;
1; Mismatches 0;
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Sequence 16, Application US/09313942

; Sequence 16, Application US/09313942

; Publication No. US20020012962A1

; Publication No. US20020012962A1

; GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
APPLICANT: REGENERON PHARMACEUTICALS, INC.
ITITLE OP INVENTION: AND USING
FILE REFERENCE: REG 203-A

; FILE REFERENCE: REG 203-A

; CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR PHICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PASCSEQ for Windows Version 3.0

SEQ ID NO 16
LENGTH: 315
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ORGANISM: Homo sapiens
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                                             PHSWNSSFYRLRFELRYRAERSKTFTTWWVKDLQHHCVIHDAWSGLRHVVQLRAQBEFGQ
                                                          PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLOHHCVIHDAWSGLRHVVQLRAQEEFGQ
 GEWSEWSPEAMGT
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                                                                                                                                                                                                                                                                                             Score 1683; DB 9;
Pred. No. 4.5e-122;
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ANTAGONISTS,
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                                                                                                                                                                                                                                                                                                           Length 315;
                                                                                                                                                                                                                                                                                        Indels
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RESULT 20 US-09-935-868-16

Sequence 16, Application US/09935868 Patent No. US20020164690A1

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GENERAL INFORMATION:

APPLICANT: Neil Stahl and George D. Yancopoulos

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203DA.

CURRENT PILING DATE: 2002-11-01

PRIOR PILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: USSN 09/935,868

PRIOR FILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: USSN 09/787,835

PRIOR APPLICATION NUMBER: USSN 09/313,942

PRIOR PILING DATE: 1999-05-19

PRIOR PILING DATE: 1999-05-19

PRIOR PILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 05/101,858

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR APPLICATION NUMBER: 60/101,858
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APPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Receptor Based Antagonists, and
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 315
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US-10-287-035-16
US-10-287-035-16
; Sequence 16, Application US/10287035
; Publication No. US20030104567A1
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LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
-10-287-035-16
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ORGANISM: Homo sapiens
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Pred. No. 4.5e-122;
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Sequence 16, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF INTERFERENCE: REG 203-B-US
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
TENCATU- 116
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Best Local Similarity 99.7
Matches 312; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      LENGTH: 315
TYPE: PRT
ORGANISM: Homo
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                                                                                                                                                                              CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
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                      PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240
                                                                                                                     VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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PEGDSSFYIVSMCVASSVGSKFSKTQTTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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Pred. No. 4.5e-122;
                                                                                                                                                                                                                                          Score 1683; DB 14;
Pred. No. 4.5e-122;
1. Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 141; LENCTH: 387
TYPE: PRT; ORGANISM: Mus musculus
US-10-322-696-141
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US-10-322-696-141
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Publication No. US20040166490A1
GENERAL INFORMATION:
                                                                                                                                                                     RESULT 24
US-10-247-463-13
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Best Local
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APPLICANT: Malandro, Marc
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 529452001200
CURRENT APPLICATION NUMBER: US/10/322,696
CURRENT FILING DATE: 2003-10-17
RUMBER OF SEQ ID NOS: 186
                                                                                                               Sequence 13, Application US/10247463
Publication No. US20030082734A1
GENERAL INFORMATION:
APPLICANT: Dowling, Lynette M.
APPLICANT: Timans, Jacqueline C.
APPLICANT: Gorman, Daniel M.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
TITLE OF INVENTION: Methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA 179
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                                                                                                                                                                                                                                                                           MPVPPGEDSKDVAAP 373
                                                                                                                                                                                                                                          --LAPVQESSSMSLP 365
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APPLICANT: MOOD, WILLIAM I.

APPLICANT: MOOD, WILLIAM I.

APPLICANT: WOOD, WILLIAM I.

FILE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES

FILE REFERENCE: P1381R1C2

FILE REFERENCE: P1381R1C2

CURRENT APPLICATION NUMBER: US/09/854,280

CURRENT FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: US 09/311,832

PRIOR FILING DATE: 1998-05-14

PRIOR APPLICATION NUMBER: US 60/085,579

PRIOR APPLICATION NUMBER: US 60/085,579

PRIOR APPLICATION NUMBER: US 60/113,621

PRIOR FILING DATE: 1998-05-15

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 26

1 SEQ ID NO 14

1 SEQ ID NO 14
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ORGANISM: Homo sapiens US-09-854-280-14
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/247,463
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US/09/588,113
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Jian
APPLICANT: Filvaroff,
APPLICANT: Goddard, Au
APPLICANT: Gurney, Aus
APPLICANT: Li, Hanzhor
APPLICANT: Li, Hanzhor
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09854280 Patent No. US20020052027A1
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TYPE: PRT
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                                                   LENGTH: 212
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Gurney, Austin
Li, Hanzhong
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APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gorney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Li, Hanzhong
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
TITLE OF INVENTION: WIMBER: US/09/854,208
CURRENT APPLICATION NUMBER: US/09/854,208
CURRENT FILING DATE: 1998-05-14
PRIOR APPLICATION NUMBER: US/09/311,832
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 212
TYPE: PRT
TOCANTEM: Homo sapiens
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US-09-854-208-14
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Best Local Similarity
Matches 187; Conserv
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Best Local Similarity
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202
                                                                                                                                                                                                                                                                       354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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                                                                                                 AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
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                                                                         AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
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LOSSLRALROM 212
                                  LOSSLRALROM 543
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                                                                                                                                                                                                                                                                                                           Score 938.5; DB 9
Pred. No. 1.5e-64;
0; Mismatches 3
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Pred. No. 1.5e-64;
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RESULT 27

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Sequence 13, Application US/10400377

Publication No. US20030162949A1

GENERAL INFORMATION:
APPLICANT: COX III, George N

APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS

CURRENT APPLICATION NUMBER: US/10/400,377

CURRENT FILING DATE: 2003-03-26

PRIOR APPLICATION NUMBER: US/09/462,941

PRIOR APPLICATION NUMBER: 60/052,516

PRIOR FILING DATE: 1907-07-14

VUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 13

LENGTH: 212

TYPE: PRT
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Publication No. US20030017150A1
GENERAL INFORMATION:
APPLICANT: Theodore Torphy
TITLE OF INVENTION: DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN-0286
FILE REFERENCE: CEN-0286
CURRENT APPLICATION NUMBER: US/10/099,007A
CURRENT PILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 17
SOOTWARB: Patentin Ver 2.0
SEQ ID NO 3
LENGTH: 212
TYDE: DET
                                                                                                                                                         Query Match 32.8%;
Best Local Similarity 97.9%;
Matches 187; Conservative
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ORGANISM: Homo sapiens
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                     KEALAENNLINLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
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KEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
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                                                                                                                                                         Score 938.5; DB 14; Length 212; Pred. No. 1.5e-64; 0; Mismatches 3; Indels 1;
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APPLICANT: COX III, George N
APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/400,708
CURRENT FILING DATE: 2003-03-26
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR PILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1097-07-14
NUMBER OF SEQ ID NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 13
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
US-10-400-708-13
APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILTE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/298,148
CURRENT FILING DATE: 2002-11-15
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 212
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US-10-400-708-13
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US-10-298-148-13
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Best Local S
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Publication No. US20030171284A1
GENERAL INFORMATION:
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nes 187; Conservative
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pred. No. 1.5e-64;
0; Mismatches 3
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APELICANT: OF PRIMO, SAMUEL
APPLICANT: OF PRIMO, SAMUEL
APPLICANT: OF PARREIL, ANNE-MARIE
APPLICANT: MORIMOTO, ALYSSA
APPLICANT: MORIMOTO, ALYSSA
APPLICANT: MANNING, WILLIAM
APPLICANT: MANNING, WILLIAM
APPLICANT: MANNING, WILLIAM
APPLICANT: MANNING, WILLIAM
APPLICANT: SCHILLING, JUM
TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
TITLE OF INVENTION NUMBER: 60/380,872
PRIOR APPLICATION NUMBER: 60/380,872
PRIOR APPLICATION NUMBER: 60/448,972
PRIOR APPLICATION NUMBER: 60/448,972
PRIOR APPLICATION NUMBER: 60/448,874
PRIOR APPLICATION NUMBER: 60/448,872
PRIOR APPLICATION NUMBER: 60
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; ORGANISM: HOT
US-10-298-148-13
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; Publication No. US200
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Homo sapiens US-10-440-464-61
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Best Local Similarity
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413 KEALAENNLNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
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vo. US20040018528A1
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pred. No. 1.5e-64;
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Pred. No. 1.5e-64;
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533 LOSSLRALROM 543

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APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
FILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/774,149
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/400,377
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1097-07-14
PRIOR FILING DATE: 1997-07-14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 212
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Sequence 13, Application US/10774149

Publication No. US20040175800A1
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US-10-773-939-13
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; SOFTWARE: PATENTIN VEY. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-773-939-13
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APPLICANT: COX III, George N
APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.

TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/773,939
CURRENT FILING DATE: 2004-02-05
CURRENT FILING DATE: 2004-02-05
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Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-14
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ilarity 97.9%;
Conservative
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Publication No. US20040214287A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/773,654
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/400,377
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1997-07-14
NUMBER: OF SEQ ID NOS: 41
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Best Local Similarity
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Best Local Similarity
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                                    LOSSLRALROM 543
                                                                                                    AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF 532
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LOSSLRALROM 212
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97.9%;
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Pred. No. 1.5e-64;
0; Mismatches 3;
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Pred. No. 1.5e-64;
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RESULT 35 US-10-828-343-3 ; Sequence 3, Application US/10828343

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Publication No. US20040228838A1
GENERAL INFORMATION:
APPLICANT: FLECKENSTEIN, Bernhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/828,343
FILING DATE: 21-Apr-2004
CLASSIFICATION NUMBER: US/09/230,048
APPLICATION NUMBER: US/09/230,048
APPLICATION NUMBER: WO PCT/EP96/03199
APPLICATION NUMBER: WO PCT/EP96/03199
APPLICATION NUMBER: WO PCT/EP96/03199
APPLICATION NUMBER: WO PCT/EP96/03199
APPLICATION NUMBER: 33,683
AFTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 058315/0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
INFORMATION SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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   RESULT 36

US-10-866-540-13

; Sequence 13, Application US/10866540

; Publication No. US20040230040A1

; GENERAL INFORMATION:
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Best Local Similarity
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ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                      413
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                                                                                                                                                                                                                                                                                                                                                       22 LPAAFPAPVPPGEDSKOVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                             KBALAENNINI-PKMAEKOGCFOSGFNEETCLYKIITGILEFEVYLEYLQNREESSEEQAR 472
                                                                                                                                                                                                                                                                                KEALAENNLNLÉKMAEKDGCFOSGFNEETCLVKI ITGLLEFEVYLEYLONRÉESSEEOAR 141
                                                                                                                                                                                                          AVQMSTKVLÍQFLQKKÁKNÍDÁÍTTÞÞÞTTNÁSLÍTKLQÁQNQMLQDMTTHLÍLKSFKEF
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                                                                                                                                   LOSSLRALROM 212
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nilarity 97.9%;
Conservative
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HUANG, Yao-Qi
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NEIPEL, Frank
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Pred. No. 1.5e-64;
0; Mismatches 3
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APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/866,540
CURRENT FILING DATE: 2004-06-10
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/10/400,377
PRIOR FILING DATE: 2003-03-26
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR APPLICATION DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 13
LENGTH: 212
                                                                                                                                                                                                                                                        APPLICANT: Ralph, Stephen John
APPLICANT: Ralph, Stephen John
ITITE OF INVENTION: IMMUNE POTENTIATING COMPOSITIONS
FILE REFERENCE: DAVIZOO.001APC
FURRENT APPLICATION NUMBER: US/10/276,642
CURRENT APPLICATION NUMBER: PCT/AU01/00565
PRIOR APPLICATION NUMBER: PCT/AU01/00565
PRIOR APPLICATION NUMBER: PCT/AU01/00565
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: PQ 7553
PRIOR APPLICATION NUMBER: PQ 7553
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 20
SOPTMARE: FRETSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 212
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US-10-276-642-6
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Publication No. US20040235156A1
GENERAL INFORMATION:
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                                                                                                                                    Matches
                                                                                                                                Best Local Similarity Matches 187; Conserv
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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al Similarity 97.9%;
187; Conservative
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413 KEALAENNINIPKWAEKDGCFOSGFNEETCLVKIITGLLEFEVYLEVLQNRFESSEEQAR 472
                                                                            354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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                                                              32.8%;
milarity 97.9%;
Conservative (
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pred. No. 1.5e-64;
0; Mismatches 3
                                                                                                                                            0;
                                                                                                                                          Score 938.5; DB 17;
Pred. No. 1.5e-64;
0; Mismatches 3;
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RESULT 39
US-10-083-446-145
; Sequence 145, Applicatior
; Publication No. US200301;
Publication No. US200301
TENERAL INFORMATION:
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Publication No. US20040215008A1
GENERAL INFORMATION:
APPLICANT: Biochemie Gesellschaft m.b.H.
TITLE OF INVENTION: Production of proteins
FILE REFERENCE: G-31109/A/BER
CURRENT APPLICATION NUMBER: US/10/763,619
CURRENT FILLING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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US-10-763-619-8
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Best Local Similarity
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligo-histidine purification aid combined with OTHER INFORMATION: sequences of Pestivirus and Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 347
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                                                                                                                                                                                       RSFKEFLOSSLRALROM 347
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                                                                                                                                                                                                                                                                                                  Application US/10083446
b. US20030185790A1
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Bauer, S. C.
Braford-Goldberg,
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Pred. No. 4.4e-64;
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  RESULT 40
US-10-053-355A-3
; Sequence 3, Application US/10053355A
; Publication No. US20030077824A1
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APPLICATION UNMBER: 08/762,227

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/446,872

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C-2790/6

TELEPHONE: (636)737-6257

TELEPHONE: (636)737-6257
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                             517
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STATE: Missouri
COUNTRY: USA
                                                                                                                                             LQDMTTHLILRSFKEFLQSSLRALRQM 543
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                                                                                                                                                                                                                           LEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQW
                                                                                                                                                                                                      LEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQW
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FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                        LODMITHLILRSFKEFLOSSLRALROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 317 amino acids
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Pred. No. 5e-64;
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Page 16
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APPLICANT: ROSS:, Alex APPLICANT: ROSS:, Alex APPLICANT: ROSS:, Alex APPLICANT: RURNITON: Small Molecule Drug Discovery TITLE OF INVENTION: Small Molecule Drug Discovery TYPLE PRICE TO APPLICATION NUMBER: US/10/053,355A CURRENT FILING DATE: 2002-06-18 ERGOR PELLING DATE: 2001-08-31 PRIOR	C . 70	но	B 8	유양	유 성		di
TION:  \$i, Alex TION: Production of Cultured Human Mast Cells and Basophils TION: Production of Cultured Human Mast Cells and Basophils TION: Small Molecule Drug Discovery  :: A-70882/RMS/AMS ATION NUMBER: US/10/053,355A  :DATE: 2002-06-18 :ION NUMBER: US 60/316,723  ID NOS: 42 :IN NOS: 42 :IN NOS: 42 :IN NOS: 42 :IN THE PROPERTY OF	Sear Job	ਲਵ	ъ ч	σ κ	0 ~	Que Bes Mat	APP TIIT TIIT TIIT FIII CUF CUF PRIIT PRII
TION:  \$i, Alex TION: Production of Cultured Human Mast Cells and Basophils TION: Production of Cultured Human Mast Cells and Basophils TION: Small Molecule Drug Discovery  :: A-70882/RMS/AMS ATION NUMBER: US/10/053,355A  :DATE: 2002-06-18 :ION NUMBER: US 60/316,723  ID NOS: 42 :IN NOS: 42 :IN NOS: 42 :IN NOS: 42 :IN THE PROPERTY OF	cin					che T	RALICE RALICE TERMINE RALICE RENTER REPORTED RENTER REPORTED RENTER REPORTED RENTER REPORTED RENTER REPORTED RENTER REPORTED RENTER REAL RENTER RENTER REAL RENTER
TION:  \$i, Alex TION: Production of Cultured Human Mast Cells and Basophils TION: Production of Cultured Human Mast Cells and Basophils TION: Small Molecule Drug Discovery  :: A-70882/RMS/AMS ATION NUMBER: US/10/053,355A  :DATE: 2002-06-18 :ION NUMBER: US 60/316,723  ID NOS: 42 :IN NOS: 42 :IN NOS: 42 :IN NOS: 42 :IN THE PROPERTY OF	: e o				w	G P	ANT OF OF APPER AP
TION:  \$i, Alex TION: Production of Cultured Human Mast Cells and Basophils TION: Production of Cultured Human Mast Cells and Basophils TION: Small Molecule Drug Discovery  :: A-70882/RMS/AMS ATION NUMBER: US/10/053,355A  :DATE: 2002-06-18 :ION NUMBER: US 60/316,723  ID NOS: 42 :IN NOS: 42 :IN NOS: 42 :IN NOS: 42 :IN THE PROPERTY OF	р1е 19	540 181				24.8	FOR : R INV
Small Molecule Drug Discovery  10882/RMS/AMS  10811 MOLECULE Drug Discovery  10882/RMS/AMS  1001-06-18  1001-06-18  1001-06-31  1001-08-44  1001-08-44	ted 3.4	FR FR	된드된	NLT N	PVP 	im.	MAT: oss: ENT CC: CC: ICA
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Molecule Drug Discovery  %5/AMS 8: US/10/053,355A 2-06-18 US 60/316,723 8-31 n 3.1 n 3.1  n 3.1  pred. No. 2.8e-64; pred. No. 2	ecen	84	ÖKK — ÖKK	MAE:	DSKI 	ery Lty	Alex Alex Pi Pie Pie Pie
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Q92p15 rhizobium m
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P96289 mycobacteri
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Score 46; DB 2; Length Pred. No. 22; ; Mismatches 1; Inde	 x_DNA_bnd. ; 77DF5D6C2F279C20 CRC64;	Monks D.B., Kitajim (G.E., Almeida N.F. Karp P.D., Bovee D rage G., Gillet W., Clelland E., Palmier Clelland E., Romero ak C., Wu Z., Romero ak C., Wu Z., Romero ak C., Jung M., Krespan lendrick C., Zhao Z., ", Gordon M.P., Olso engineer Agrobacter	RELIMINARY; PRT; 382 AA.  TrEMBLrel. 21, Created)  TrEMBLrel. 26, Last sequence update)  TrEMBLrel. 26, Last annotation update)  al regulator, ROK family.  ames=Atu4567;  tumefaciens (strain C58 / ATCC 33970).  tumefaciens (strain C58 / ATCC 34070).  teobacteria; Alphaproteobacteria; Rhizobiales  Rhizobium/Agrobacterium group; Agrobacterium  5299;	AAS53492 O9KPUT O7TMM1 O8CT51 O8CT51 O9VX34 DD10_HUMAN O80Y44 DD10_HUMAN O8SKV5 O9SKV5 O9SKV5 O9SKA5 ALIGNMENTS
382; els 0; Gaps 0	•	Jr., Woo L., Jr., Woo L., Sr., Grant C., ri A., Gordon D., D., Gordon D., W., Perry M., -Y., Dolan M., on M.V.,	elales;	Aas53492 ashbya go O9kpj7 vibrio chol O7tmm1 mus musculu O8c751 mus musculu O8c752 mus musculu O8c762 mus musculu O96v76 homo sapien O9vx34 drosophila O13206 homo sapien O80y44 mus musculu O9skv5 arabidopsis O9zkb6 rhizobium m O7r218 giardia lam O89dd4 bradyrhizob O9zka5 helicobacte

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                            SEQUENCE OF 1-127
MEDLINE=83246546;
Shen S., Xue Z., I
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MEDLINE=93247479;
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Beynon J.;
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MEDLINE=89094839; PubMed=3062178;
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2323-2328 (2001).
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Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR009051; Helical ferredxn.
InterPro; IPR009051; Helical ferredxn.
InterPro; IPR0092869; POR.
InterPro; IPR009389; POR.
InterPro; IPR009399; Pyruvate decarb.
InterPro; IPR009314; Transketo_C_like.
Pfam; PF00037; Per4; 2.
Pfam; PF01855; POR; 1.
                                                                     Ashbya gossypii (Yeast) (Bremothecium gossypii).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Bremothecium.
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PIR; S
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FUNCTION: Oxidoreductase required for the transfer of ele from pyruvate to flavodoxin, which reduces nitrogenase.
CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized flavodoxin
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SIMILARITY: The iron-s
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Iron-sulfur 1 (4Fe-4S)
Iron-sulfur 2 (4Fe-4S)
Iron-sulfur 2 (4Fe-4S)
Iron-sulfur 2 (4Fe-4S)
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                                                                                                                   Q9RS23 PRELIMINARY;
Q9RS23;
01-MAY-2000 (TrEMBLrel. 13, Cr
01-MAY-2000 (TrEMBLrel. 13, La
01-MAR-2004 (TrEMBLrel. 26, La
Hypothetical protein DR2304.
OrderedLocusNames=DR2304;
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23-APR-2004
23-APR-2004
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"The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome.";
Science 304.304-307(2004).
EMBL: AE01689; AAS53185.1; -.
                                                                                                                                                                                                                                                                                                                                                  "The Ashbya gossypii genome as a tool Saccharomyces cerevisiae genome."; Science 304:304-307(2004).
EMBL; AE016899; TASS3165.1; -
SEQUENCE 160 AA; 17720 MW; 3852786
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 STRAINARI / ATCC 13939 / DSM 20539 / NCIB 9279;

STRAINARI / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE=2036896; PubMed=10567266;

White O., Elsen J.A., Heidelberg J.F., Hickey E.J.

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=ATCC 10895;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15001715;
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., S
Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier
Gaffney T.D., Philippsen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=33169;
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                                                                     NCBI_TaxID=1299;
                                                                                                 Bacteria; Deinococcus-Thermus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Boffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Boffard N., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Korrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellens S., Potier S., Richard G., Ozier-Kalogeropoulos O.,
Pellens S., Potier S., Richard G., Ozier-Kalogeropoulos O.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincher P., General T., Wessenbach J.,
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Chromosome C of strain CLIB99 of Yarrowia lipolytica.
                                                                                                                                                                                                                                                                                                 Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382129; CAG82066.1; -.
SEQUENCE 540 AA; 58440 MW; BCC2AE9995C981AF CRC64;
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Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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Science 286:1571-1577(1999).
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8; Conserv
EFGAKIVLGGK 352
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396 AA; 39229 MW; 355FCB5E0179F312 CRC64;
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88.9%;
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Pred. No. 1.1e+02;
0; Mismatches 1
                                                                                                                                                                                                               Score 42; DB 2;
Pred. No. 1.5e+02;
                                                                                                                                                                        Mismatches
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O., Venter J.
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A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
A Godzie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
T "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
R EMBL, AL591789; CAC45561.1;
PROG. 05:0016021; C:integral to membrane; IEA.
Complete proteome; Hypothetical protein; Transmembrane.
SEQUENCE 155 AA; 17944 MW; 0A3B12286D1FDAFA CRC64;
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Best Local
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gerany-Jerany-L pyrophosphate synthase.
Name=ispA; OrderedLocusNames=CT628;
Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae;
SEQUENCE FROM N.A.
STRAIN=D / UW-3 / Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.
Mitchell W.P., Olinger L., Tatusov
                                                                                                                                                                                                                          084633;
01-NOV-1998
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Galibert F., Finan T.M., Long S.R., Buehler A., Abola P., Ampe F.,

Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,

Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,

Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,

Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,

Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,

Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,

Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,

Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,

Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;

"The composite genome of the legume symbiont Sinorhizobium meliloti.";

Crianca 201.626-677770.11
                                                                                                 NCBI_TaxID=813;
                                                                                                                                                                                                                                                             084633
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
HYPOTHETICAL TRANSMEMBRANE SIGNAL PEPTIDE PROTEIN.
OrderedLocusNames=R01982; ORTNames=SWc04336;
Rhizobium mellloti (Sinorhizobium mellloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Q92P15;
Q1-DEC-2001
01-DEC-2001
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66.7%;
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3; Mismatches
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Pred. No. 71;
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     R.L.,
                                                                                                                   Chlamydiaceae; Chlamydia
     Fan J.,
.., Zhao (
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     Marathe R.,
Q., Koonin E.
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Best Local
                                                                                                                                                                                                                                                                                                  "The sequence of a 54.7 kb fragment of yeast chromosome XV reveals presence of two tRNAs and 24 new open reading frames.";
Yeast 13:379-390(1997).
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01-NOV-1997
01-NOV-1997
                                                                                                            EMBL; U46033; AAB37236.1;
EMBL; Z74987; CAA99272.1;
EMBL; Z70678; CAA94564.1;
PIR; S66962; S66962.
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            Lin S.-J., Culotta V.C.;
"Suppression of oxidative damage by Saccharomyces cerevisiae which encodes a manganese-trafficking protein that localizes like vesicles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
Metal homeostasis factor ATX2.
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PROSITE; PS00723; POLYPRENYL SYNTHET 1;
PROSITE; PS00444; POLYPRENYL SYNTHET 2;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis.",
Science 282:754-759(1998).
EMBL; AE001333; AAC68232.1;
PIR; E71491; E71491
GO; GO:0008299; P:isoprenoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97042460; PubMed=8887660;
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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InterPro; IPR008949; Terpenoid
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S66962; SUCCEPT 143667; -.

NONLINE; 143667; -.

; S0005605; ATX2.

GO:0000139; C:Golgi membrane; IDA.

GO:00005384; F:manganese ion transporter activity;

; GO:0030026; P:manganese ion homeostasis; IGI.

TER003689; Zn_transpt_Zip.
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Pred. No. 1.2e+02
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AAS56363;
25-MAR-2004
25-MAR-2004
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Q82N27;
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cerevisiae ORFs in the Gateway recombinational Submitted (FEB-2004) to the EMBL/GenBank/DDBJ EMBL, AYSS8037; AMS56363.1; -. SEQUENCE 313 AA; 34408 MW; 81DAEFB0E469226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., H
                                        SEQUENCE FROM N.A. STRAIN=MA-4680;
                                                                                                                          Streptomycineae;
                                                                                                                                         Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                 Putative sugar kinase.
OrderedLocusNames=SAV1476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system.";
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25-MAR-2004 (TrEMBLrel.
25-MAR-2004 (TrEMBLrel.
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                                                                                                                          Streptomycetaceae;
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Pred. No. 1.3e
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  Hanamoto
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  Takahashi C.,
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Dafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Gaffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Gaffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P. Schmeis J. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp|(010067 Saccharomyces cerevisiae YOR079c
homeostasis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitils."; Nat. Biotechnol. 21:526-531(2003). EMBL, AP005027; BAC69186.1; -GO; GC:0016301; F:kinase activity; IEA. InterPro; IPR000600; ROK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00480; ROK; 1.
PROSITE; PS01125; ROK; 1.
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                                                                               EMBL;
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Candida glabrata (Yeast) (Torulopsis glabrata).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                Bouchier C., Caudron B., Scarp, Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=CAGLOK05577g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                      e 430:35-44(2004).
CR380957; CAG61429.1; -.
Pro; IPR003689; Zn_transpt_Zip.
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319 AA; 31301 MW;
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1.
36113 MW;
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Pred. No. 1.3e
0; Mismatches
  F8337EFFDDF1B0E0 CRC64;
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Query Match Best Local Similarity

61.2**%**; 53.8**%**;

Score 41; Pred. No.

1.4e+02;

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Length 331;

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Matches 8
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C STRAIN=ATCC 15692 / PAO1;

C STRAIN=ATCC 15692 / PAO1;

X MEDLINE=20437337; PubMed=10984043;

X MEDLINE=20437337; PubMed=10984043;

A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener A. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro A. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan A. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

T "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";

Nature 406:959-964 (2000).
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PIR; D83605; D83605.

HSSP; P31133; 1A99.

GO; GO:0030288; C:periplasmic space (sensu Gr. GO; GO:0005215; F:transporter activity; IEA. GO; GO:0006810; P:transport; IEA.

InterPro; IPR006059; SBP_bac_1; Dutr-bndng.

Pfam; PF01547; SBP_bac_1; 1.
                                                                                                                                                                                                                                                          Q74EW6;
Q74EW6;
05-JUL-2004 (T
05-JUL-2004 (T
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NADH oxidase;
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Q916G8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable binding protein component of ABC transporter.
OrderedLocusNames=PAG323;
                                                                                                                                                                Geobacter sulfurreducens. Bacteria; Proteobacteria; Geobacteraceae; Geobacter
STRAIN-PCA / ATCC 51573;
STRAIN-PCA / ATCC 51573;
PubMed=14671304; DOI=10.1126/science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T.,
                                                                                                                                                                                                                                           ORFNames=GSU0843;
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PRINTS; PR00909; SPERMDNBNDNG.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                       SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=35554;
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(TrEMBLrel.
se, putative.
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Pred. No. 1.5e+02;
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D.J., Lagrou M.,
n S., Yuan Y.,
K., Lim R.M.,
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RN GEODA
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InterPro; IPR00103; PyrIdine_redox_2.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox_dim.
Pfam; PF00070; Pyr_redox; 1.
Pfam; PF00070; Pyr_redox; 1.
Pfam; PF002852; Pyr_redox; 1.
PRINTS; PR00368; FADBUR.
PRINTS; PR00469; PADRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
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02-MAR-2004
02-MAR-2004
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AAR34173;
                                                                                                                                                                                                Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Maddupu R., Brinkac L.M., Daugherty S.C., DeBoy R. T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.;
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=PCA / ATCC 51573;
PubMed=14671304;
                                                                                                                          SEQUENCE
                                                                                                                                       EMBL; AE017209; AAR34173.1; TIGR; GSU0843; -.
                                                                                                                                                                       Science 302:1967-1969(2003).
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Bacteria; Proteobacteria;
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EMBL; AE017180; AAR34173.1; -.
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                             EFGAGLVLGGQFM 13
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                                                                                                                                                                                                                                                                                                                                                                                                        Geobacter.
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Pred. No.
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Pred. No. 1.8e+02
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                                                                                                                          8F86F154DC054C94 CRC64;
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RESULT 17 YFE9\_YEAST

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ID Q6FPT
AC Q6FPT
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DT Simil
GN ORFNA
GO Candi
GO Sacch
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QGFPT7;
QGFPT
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V. Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GermOnline; 140107; -. SGD; S0001845; YFL049W. GO; GO:0005634; C:nucleus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 6:
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Nat. Genet. 10:261-268(1995).
-!- SIMILARITY: TO YEAST NPL6.
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MEDLINE=95400292; PubMed=7670463;
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InterPro; IPRO01410; DEAD.

InterPro; IPRO01629; DEAD_box.

InterPro; IPRO01650; Helicase_C.

Pfam; PF00270; DEAD; 1.

Pfam; PF00271; Helicase_C; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00490; HELICC; 1.

SMART; SM00490; HELICC; 1.

PROSITE; PS00039; DEAD_ATP_HELICASE; UNKNOWN_1.

ATP-Dinding; Helicase; Hydrolase.

SEQUENCE 765 AA; 87380 MW; A0FDB5B79E63504B
                                      MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Fraser C.M.; Wikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., "Whole C.M.";
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                                                                                                                                                                                                    Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    996289;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
01-OCT-2004 (Rel. 45, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative membrane protein mmpL7.
Name=mmpL7; OrderedLocusNames=Rv2942,
ORFNames=MTCY24G1.07c;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SPECIES=M.tuberculosis; STRAIN=H37RV;
MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
                               "Whole-genome comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1773,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterineae; Mycobacteriaceae;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Wincker P., Souciet J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Genome evolution in yeasts.";
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                strains.";
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   184:5479-5490(2002).
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                            of Mycobacterium tuberculosis
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Pred. No. 2.9e
3; Mismatches
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                                 clinical
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STRAIN=PCC 7421;

MEDLINE=22977040; PubMed=14621292;

Makamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya Nakamura Y., Kaneko T., Kawashima K., Kishida Y., Kiyokawa C., Sasamoto S., Watanabbe A., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                          Q7NJE3;
Q7NJE3;
Q1-MAR-2004
01-MAR-2004
01-MAR-2004
                                                                                                                     Gloeobacter violaceus.
Bacteria; Cyanobacteria; Chroococcales; Gloeobacter
                                                                                                                                                  OrderedLocusNames=gll1889;
                                                                                                                                                             Gll1889 protein.
                                                                                                                 NCBI_TaxID=33072;
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SPECIES-M. bovis; STRAIN=AF2122/97;

SPECIES-M. bovis; STRAIN=AF2122/97;

MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Manseor H.,

Pryor M., Duthby S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Pryor M., Duthby S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Pryor M., Duthby S., Grondin S., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003)

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content entities requires a license agreement (See http://www.isb-gor.send an email to license@isb-sib.ch).
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EMBL; BA007123; AAK47339.1; -.
EMBL; B4848344; CAD96654.1; -.
PIR; C70668; C70668.
TIGR; MT3012; -.
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PF03176; MMPL; 1.
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Wu X., Wang Y., Zhou K., Zhu W., Nie J., Wang C., Submitted (MAY-2002) to the EMBL/GenBank/DDBJ dat EMBL, AF511507; AAN84928.1; -. GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:0008137; F:NADH dehydrogenase (ubiquinone GO; GO:0006120; P:mitochondrial electron transpo R InterPro; IPR001457; Oxidored q3.

R Pfam; PF00499; Oxidored q3; 1.
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OBHG38;
O1-MAR-2003 (TrEMBLrel. 23, Cre.
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'""" Ahvdrogenase submit 6.
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Archaea; Euryarchaeota; Ther
Picrophilaceae; Picrophilus.
NCBI TaxID=82076;
                                                                                                                                                                                                                                                                      Q6L0E6;
Q6L0E6;
05-JUL-2004
                                                                                                                    OrderedLocusNames=PTO0971;
Picrophilus torridus.
                                                                                                                                                                    05-JUL-2004 (TrEMBirel 27, Cr
05-JUL-2004 (TrEMBirel 27, La
05-JUL-2004 (TrEMBirel 27, La
Translation initiation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion.
SECUENCE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADH dehydrogenase
Alligator sinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=38654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylidae; Alligatorinae; Alligator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion.
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PROSITE; PS50005; TPR; 6.
PROSITE; PS50293; TPR REGION; 1.
Complete proteome.
SEQUENCE 999 AA; 109847 MW;
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InterPro; IPR001440;
Pfam; PF00515; TPR; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyanobacterium that lacks thylakoids.", DNA Res. 10:137-145(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete
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9; Conserv
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8; Conserv
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                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                sequence update)
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databases.
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                                                                         XX SEDLINE=22386257; PubMed=12477932;
XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
XX Strausberg R.L., Feingold E.A., Grouse I.H., Derge J.G.,
XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
XX Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
XX Altechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altechenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Altechenko L., Wagner M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Altechenko L., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altechenko M.J., Schmut S., Garcia A.M., Schmit J., Wyers R.M., Butterfield Y.S.,
XX Altechenko M.J., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
XX Altechenko M.J., Schmit D.E., Schmerch A., Schein J.E.,
XX Altechenko M.J., Schmit J., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
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Best Local S
Matches
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Q7ZSZ2;
Q1_JUN-2003 (TrEMBLrel. 24, Created)
Q1_JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q5_JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Claudin,
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SMART; SM00653; eIF2B_5; 1.

PROSITE; PS50926; TRAM; 1.

Complete proteome; Initiation factor.

Complete proteome; Initiation factor.
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EMBL; AE017261; AAF43556.1; -.
GO; GO:0003743; F:translation initiation factor activity; IEA.
InterPro; IPR002735; eIF5_eIF2B.
InterPro; IPR002792; TRAM.
Pfam; PF01938; TRAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Fujita M., Itoh M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
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Schepers B., Dock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene
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Schepers B., Dock C., Antranikian G., Li
"Genome sequence of Picrophilus torridus"
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A.
                                                              Jones S.J., Marra M.A.;
                                        'Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a M., Itoh M., Shibata M., Taira S., Taira M., expression pattern analysis of the tight junci
in, in the early morphogenesis of Xenopus embry
Expr. Patterns 2:23-26(2002).
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9790 / ATCC 700027;
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Pred. No.
  99:16899-16903 (2002)
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., Liebl W.;
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cches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi; ia; Pipoidea; Pipidae;
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                                        full-length
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Best Local
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ dat
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ dat
EMBL; BR072910; BAC21015.1; -.
EMBL; BC048771; AAH48771.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005193; C:tight junction; IEA.
GO; GO:0005193; F:structural molecule activity;
InterPro; IPR006187; Claudin.
InterPro; IPR006187; Claudin.
InterPro; IPR006188; Claudin.
InterPro; IPR006188; Claudin.
InterPro; IPR006189; Claudin.
InterPro; IPR006189; Claudin.
Pfam; PF00022; PMP22 Claudin; 1.
                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Phosphoadenosine phosphosulfate reductase (EC 1.8.4.8) (PAF reductase, thioredoxin dependent) (PAGOPS reductase) (3'-phosphoadenylylsulfate reductase) (PAPS sulfotransferase).
                                                                                                                                                                                                                                                                                                                                         MEDLINE=93099269; PubMed=1463852; Niehaus A., Gisselmann.G., Schwenn J.D.; Primary structure of the Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-cysH; Synonyms-par, sea0019;
Synechococcus sp. (strain PCC 7942) (Anacystis nidulans
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                           Holtman C.K.,
                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                    "Primary structure gene.";
Plant Mol. Biol. 20
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYSH_SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01346; CLAUDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01077; CLAUDIN. PRINTS; PR01381; CLAUDIN7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22341132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic and
                                                                                                                                                                                                                                                                                                 ant Mol. Biol. 20:1179-1183(1992)
  branch; third step.
SUBCELLULAR LOCATION: Cytoplasmic (By SIMILARITY: Belongs to the PAPS reduct
                                                                      PATHWAY: Sulfate activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dyn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFGAGLVLG--GQFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFGAGVFLGWAGSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225:384-391 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                     N.A.
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                                                                                                                                                                                                                                Socias T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22731 MW;
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                                                                                                                                                                                                                             Mohler B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174
       the PAPS reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB
Pred. No. 1.4e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDDF3E2D804B5775 CRC64;
                                                                      cysteine
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U.,
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                                                                                                                                                                                                                                  Chen Y.,
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ches 2;
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                                                                                                                                                                                                                                                                                                                                                224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                              similarity)
                                                                        biosynthesis
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                                                                                                                                                                                                                                  u;E
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                                                                                                                                                                                                                                                                                                                                                PAPS
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         CysH subfamily.
                                                                          reductive
                                                                                                                                                                                                                                  Golden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PAPS
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RESULT 25
Q8KMM1
ID Q8KMM
AC Q8KMM
DT 01-MA
DT 0
   RESULT 26
CAD24411
ID CAD24
AC CAD24
DT 12-MA
DT 12-MA
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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EMBL; U30252; AAL03931.1; -.
PIR; S28609; S28609.
HSSP; P17854; ISUR.
HAMAP; MF 00063; -; 1.
InterPro; IPR004511; cysH.
InterPro; IPR004511; cysH.
InterPro; IPR004511; cysH.
InterPro; IPR004511; cysH; 1.
TIGRPAMS; TIGR00434; cysH; 1.
TIGRPAMS; TIGR00434; cysH; 1.
Cysteine biosynthesis; Oxidoreductase.
CONFLICT 218 218 T -> S (in Ref. 2)
CAD24411;
CAD24411;
12-MAY-2004
12-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8KMM1;
Q8KMM1;
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8KMM1;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helanto M.E.K., Airaksinen U., von Weymarn N., Submitted (FEB-2002) to the EMBL/GenBank/DDBJ of EMBL, AJ431694; CAD24411.4; -.
GO; GO:000865; F:fructokinase activity; IEA.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00480; ROK; 1.
PROSITE; PS01125; ROK; UNKNOWN_1.
Kinase; Transferase.
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Bacteria; Firmicutes; Lactobacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000600;
                                                                                                                                                                                                                                                                                                 136
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                                                                                                                                                                                                                                                                                                                                                             3 GAGLVLGGQFM 13
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
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8; Conserv
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GAGIVSGGRFV 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
(TrEMBLrel.
                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.7%;
63.6%;
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27,
27,
Created)
Last sequence update)
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2;
                                                                                                          PRT;
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549FFECCB3BF8F7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 1.8e+02;
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RESULT
O31016
ID
RESULT 28
FABH TROWT
ID FABH T
AC Q83HL5
DT 10-OCT
DT 10-OCT
DT 05-JUL
DE 3-OXOA
DE ketoac
GN Name=f
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Matches 7
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Best Local S
Matches 7
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O1.7JAN-1998 (TrEMBLrel. 05, Cre.
O1.7JAN-1998 (TrEMBLrel. 05, Las.
O1.7UN-2003 (TrEMBLrel. 24, Las.
Putative rhamnosyl transferase.
                                                                 FABH TROWT STANDARD; PRT; 3
Q83HL5; Q83N01;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jedani K.E., Stroeher U.H., Manning P.A.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
EMBL; AF025396; AAB81635.1; -.
GO; GO:0010740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mannitol production.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AJ431694; CAD24411.4; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATTC-12291;
Helanto M.E.K., Airaksinen U., von
"Characterization of random mutant
                    3-oxoacyl-[acyl-carrier-protein] synthase III ketoacyl-ACP synthase III) (KAS III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001173; Glyco trans 2.
InterPro; IPR006446; Rhamnosyltran.
Pfam; PF00535; Glycos transf 2; 1.
TIGRPAMs; TIGR01556; Thamnosyltran;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=85-3954-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=55601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Listonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio anguillarum (Listonella anguillarum)
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SEQUENCE 288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Bacteria; Fi
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     OrderedLocusNames=TWT253,
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irmicutes; Lactobacillales;
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58.3%;
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Last annotation update)
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Pred. No.
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strain of Leuconostoc
ow on fructose and its use
                                                                                           update)
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                                                2.3.1.41) (Beta-
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Matches 8
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Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
Dover L.G., Norbertczak H.T., Beara G.S., Quail M.A., Harris D.F.
von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
Barrell B.G., Parkhill J., Relman D.A.;
"Sequencing and analysis of the genome of the Whipple's disease
bacterium Tropheryma whipplei.";
Lancet 361637-644(2003)
                                                                                                                                                                                                                                                                                                                         InterPro;
TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrement of Bioinformatics and the Entre Buropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016851; AA044350.1; ALT_INIT.
EMBL; BX251411; CAD67184.1; -.
HASP; O06399; 1HZP.
HAMAP; MF_01815; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                        Acyltransferase; Complete proteome; Multifunctional enzyme; Transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Twist / Genotype 2A;
MEDLINE=22784088; PubMed=12902375; DOI=10.1101/gr.1474603;
Raoult D., Ogata H., Audic S., Robert C., Suhre K., Dranco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tropheryma whipplei (strain Twist) (Whipple's bacillus), and Tropheryma whipplei (strain TW08/27) (Whipple's bacillus). Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Tropheryma whipplei Twist: a reduced genome.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SIMILARITY: Belongs to the fabH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [acyl-carrier protein].

PATHWAY: Fatty acid biosynthesis.

SUBUNIT: Homodimer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Probable).

DOMAIN: The last Arg residue of the ACP-binding sit for the weak association between ACP/acpP and fabH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                initiates fatty acid synthesis and may therefore play a role in governing the total rate of fatty acid production. Possesses both acetoacetyl-ACP synthase and acetyl transacylase activities. Its substrate specificity determines the biosynthesis of branched-chain and/or straight-chain of fatty acids (By similarity).

CATALYTIC ACTIVITY: Acyl-lacyl-carrier protein] + malonyl-(acyl-carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Catalyzes the condensation reaction synthesis by the addition to an acyl acceptor malonyl-ACP. Catalyzes the first condensation
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                                                                     Similarity
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FGAGLVLGGQ
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TIGR00747; fabH; 1.
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247
278
248
322
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11
                                                                                                                                                34211
                                                                        59.7%;
                                                                                                                                                   ¥
                                              Score 40; DB
Pred. No. 2e+0
0; Mismatches
                                                                                                                                           By similarity.
By similarity.
By similarity.
By similarity.
ACP-binding (By similarity).
, 3A2A1E592BDF1804 CRC64;
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                                                                        2e+02;
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                                                                                             Length 322;
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RESULT TO SOLVE A SOLV
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Itoh M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsuncto H., Sakaguchi S., Kegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayyashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
enriched library, clone:B130020M16 product:DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase), full insert sequence.
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P. Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Fukuda S., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T., Konto F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kojima Y., Kondo S., Konno H., Kouda M., Koya Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium, the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8BRE3;
01-MAR-2003
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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Mammalia; Eutheria;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N. J
STRAIN=C57BL/6J;
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
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6J; TISSUE=Parthenogenote;
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Rodentia;
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Sciurognathi; Muridae;
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on functional
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; Murinae; Mus
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of new
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GO; GO:0003676; F:nucleic acid binding; IE
GO; GO:0003676; F:nucleic acid binding; IE
InterPro; IPR011545; DEAD, DEAD,
InterPro; IPR011545; DEAD, DeAH, N.
InterPro; IPR001629; DEAD, Dox.
InterPro; IPR001650; Helicase_C.
pfam; PF00270; DEAD; 1.
pfam; PF00270; DEAD; 1.
smarT; SM00480; HELICC; 1.
SMART; SM00480; HELICC; 1.
                                                                                                            Query Match
Best Local
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-i-SIMILARITY: Belongs to the DEAD box helicase family.

EMBL; AK045032; BAC32191.1; -.
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Q9A7D4 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CCT789.
OrderedLocusNames=CCT89;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SETRAINATCC 19089 / CB15;

MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Melson K.E., Eisen J.A., Ohta N., Maddock J.R., Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Ely B. Debocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B. DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J., Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J., Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Caulobacter
Proc. Natl. Acad. Sci. U.S.A. 98:4136-414
EMBL; AE005853; AAK23765.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           raser C.M.;
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GO:0005524; F:ATP binding; IEA.
GO:0008026; F:ATP-dependent helicase activity; IEA.
                                                                                                                                                                                                                                                                              A87471; A87471.
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FGAGLVLGG
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492 AA; 52155 MW; 1
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                                                                                     Conservative
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77.8%;
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Pred. No. 2.8e+02;
4; Mismatches 1
                                                                                        Score 40; DB
Pred. No. 2.9e
1; Mismatches
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1AC43E2A90950D5A CRC64;
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                                                                                                  STRAIN=ATCC 10895;

PubMed=15001715;

Dietrich F.S., Voegeli S., Brachat S
Mohr C., Pohlmann R., Luedi P., Choi
Gaffney T.D., Philippsen P.;

"The Ashbya gossypii genome as a too
Saccharomyces cerevisiae genome.";
Science 304:304-307(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q754E9;
Q754E9;
05-JUL-2004
05-JUL-2004
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23-APR-2004
23-APR-2004
                                                                                                                                                                                                                                                 AFR121Wp.
AFR121W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae genome.";
Science 304:304-307(2004).
EMBL; AE016901; AAS53492.1; -.
AGD; AFR121W; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietrich F.S., Voegeli S., Brach
Mohr C., Pohlmann R., Luedi P.,
Gaffney T.D., Philippsen P.;
"The Ashbya gossypii genome as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashbya gossypii (Yeast) (Eremothecium gossypii).
Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 10895;
PubMed=15001715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales;
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                                                                                                                                                                                                     Ashbya gossypii (Yeast) (Bremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Bremothecium.
NCBI_TaxID=33169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                   AAS53492;
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                                                                               EMBL; AE016901; AAS53492.1; -. SEQUENCE 555 AA; 65009 MW;
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                    EFGAGLVLGGQFM 13
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61.5%;
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Last annotation updat
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Pred. No.
                                                     Score 40; DB 2;
Pred. No. 3.3e+02;
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                                           Mismatches
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., Wing R.A.,
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RESULT 34
Q7TMM1
ID Q7TMM
AC Q7TMM
DT 01-OC
DT 01-MA
DE Ddx10
GN Nume-
OC Eukar
OC Eukar
OC Mamma
OC MCBI
RP SEQUE
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SMART; SM00267; DUF1; 1.
SMART; SM00086; PAC; 2.
SMART; SM00091; PAS; 2.
SMART; SM00091; PAS; 2.
TIGRFAMS; TIGR00229; Sensory_bo;
PROSITE; PS50807; GGDEF; 1.
PROSITE; PS50807; GGDEF; 1.
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STRAIN-EI TOR N16961 / Serotype O1;

MEDLINE-20406833; PubMede10952301; DOI=10.1038/35020000;

MEDLINE-20406833; PubMede10952301; DOI=10.1038/350200000;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,

Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,

Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,

Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,

Mekalanos J.J., Venter J.C., Fraser C.M.;

"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                            O7TMM1 PRELIMINARY;
07TMM1;
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; VC2370; -.
GO; GO:000155; F:two-component sensor molecule activity; IEA.
GO; GO:0000160; P:two-component signal transduction system (p.
InterPro; IPR000160; GGDEF.
InterPro; IPR001610; PAC.
InterPro; IPR000170; PAS-assoc_C.
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Q9KPJ7;
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Pfam; PF00785; PAC; 1.
                                                                                                                                               Ddx10 protein (Fragment)
Name=Ddx10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 579 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:477-483(2000).
EMBL; AE004307; AAF95513.
PIR; B82085; B82085.
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SEQUENCE FROM N.A
                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                         Mus musculus (Mouse)
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8; Conserv
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                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.7%;
88.9%;
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Pred. No.
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                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                 sequence update) annotation updat
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RESULT 35
Q8C751
ID Q8C75
AC Q8C75
AC Q8C75
AC Q8C75
DT 01-MA
DT 01-MS m
DT 01-OC
DB 11brs
DE 11brs
DB 12F
CN Name m
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XX MEDLINE-22388257; PubMedel12477932;

XX MEDLINE-22388257; PubMedel12477932;

XX MEDLINE-22388257; PubMedel12477932;

XX MEDLINE-2388257; PubMedel12477932;

XX MEDLINE-2388257; PubMedel12477932;

XX Maltschul S.F., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Altschul S.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

XX Altschul S.F., Jordan H., Monaldo M.F., Casavant T.L., Scheetz T.E.,

XX Altschul S.F., Loquellano N.A., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Altschul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altschul S.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altschul S.F., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Altschul S.F., McDuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altschul S.F., McDuellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,

XX Altschul S.F., McEusan M., Madan A., Rodrigues S., Sanchez A.,

XX Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Milting M., T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Alones S.T. Marra M.A.,

XX Alones S.T. McComman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,

XX Alones S.T. McComman J.W.
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Best Local S
Matches 6
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InterPro; IPR001545; DEAD/DEAH_N.
InterPro; IPR001629; DEAD_box.
InterPro; IPR001650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00480; HELICA; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
ATP-binding; Helicase; Hydrolase.
                                                                                                                                                                                                01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                  Q8C751;
                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
library, clone:D430047D13 product:DEAD/H (Asp-Glu-Ala-Asp/His) bo:
polypeptide 10 (RNA helicase), full insert sequence. (Fragment).
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   Eukaryota; Metazoa;
                                                              Name=Ddx10;
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virgin mouse. Taken by
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                                  Mus musculus (Mouse)
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DFSAGLIIGGK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               623 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70849 MW; F5B6893E71179D94 CRC64;
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Pred. No. 3.6e+02;
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C STRAIN-GS7BL/GJ; TISSUB-Lung;

RC STRAIN-GS7BL/GJ; TISSUB-Lung;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

RA Houri J., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TAGS2540; BAC35031 1; -.

C MBL; AKO52540; BAC35031 1; -.

ROJ, GO:0008524; F:ATP binding; IEA.

GO; GO:0008524; F:ATP binding; IEA.

GO; GO:000857; F:Bydrolase activity; IEA.

GO; GO:000857; F:Bydrolase activity; IEA.

BR GO; GO:003676; F:nucleic acid binding; IEA.
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Haysahizaki V.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=(57BL/6J; TISSUE=Lung;

MEDLINE=20530913; PubMed=11076861;

MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Yujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUB-Lung; MEDLINB-20499374; PubMed=11042159; MEDLINB-20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Carninci P., Shibata Y.; Muramatsu M., Hayashizaki Y.; Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria;
     IPR011545; DEAD/DEAH_N.
IPR000629; DEAD_box.
IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci P.,
                                                                                                                                                                                                                                                                                                                                                   Tagami M.
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SAKADAB
OR OF STATE 
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimsood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez S. M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S. M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S. M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S. M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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pfam; pF00271; Helicase_C; 1.
smarT; SM00487; DEXDC; 1.
smarT; SM00490; HELICC; 1.
pROSITE; PS00039; DEAD ATP_HELICASE; 1.
ATP-binding; Helicase; Hydrolase.
NON_TER 681 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8CFS2; PRELIMINARY;
Q8CFS2;
Q1-MAR-2003 (TrEMBLrel. 23,
Q1-MAR-2003 (TrEMBLrel. 23,
Q1-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ddx10 protein (Fragment).
                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:
                         JO; GO: DEAD.

InterPro; IPR001410; DEAD.

InterPro; IPR011545; DEAD/DEAH_N.

InterPro; IPR000629; DEAD_box.

InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                   GO:0003676; F:nucleic acid binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Н
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFGAGLVLGGQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77839 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.7%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; I
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF8B6EB62BB6F988 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 681 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length human
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RESULT 37
Q86VVA
ID V866VI
ID V866VI
AC Q86VI
AC Q86VI
AC Q86VI
DT 01-JU
RN EDDIJ
RN ITISSI
RA Strain
RA HOPKI
RA HORN
RA HORN
RA HORN
RA BIANK
RA BIANK
RA RAHA
RA RAHA
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RA RAHA
RA RAHA
RA BIANK
RA WALL
RA BIANK
RA WALL
RA BIANK
RA JONE
RA FAHE
RA JONE
RA GO;
DR                                                                          S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKEDLINE=2238257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
AKIausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
ALEschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
AA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
AD Liatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
AD Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
AD Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
AD Liatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
AD Liatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
AD Liatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
AD Liatchenko L., Malan M., Peters G.J., Abramson R.D., Mullahy S.J.,
AN Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunarathe P.H.,
AD Robert S.A., McCwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
AD Robert S.A., McCwan P.J., McKernan K.J., Malek J.A., Gubs R.A.,
AN Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
AN VIllalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
AN Hiting M., Madan A., Young A.C., Schechenko Y., Bouffard G.G.,
AN Hiting M., Madan A., Young A.C., Schechenko Y., Bouffard G.G.,
AN Hiting M., Touchman J.W., Green E.D., Dickson M.C.,
AN Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
An Tones S. T. Marra M. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q86VR6;
Q86VR6;
01-JUN-2003
01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00271; Helicase C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE;
ATP-binding; Helicase; Hydrolase.
NON_TER 681 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDX10 protein (Fragment).
Name=DDX10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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                           Helicase C; 1. ; DEXDc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A. 99:16899-16903(2002)
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Last annotation updat
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Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Saga
                                                              RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Lil R.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Lil R.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Holt R.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Button G.G., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Bardon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Burtis K.G., Basu A., Baxendale J., Bayraktaroglu L., Besley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Besley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brokteir P., Chandra I., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brokteis P., Chandra I., RA Borkova D., Botcher A., Deng Z., Maya A.D., Dew I., Chandra I., RA Borkova D., Botcher A., Deng Z., Maya A.D., Dew I., Chandra I., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Gebabios B., Delcher A., Deng Z., Maya A.D., Dew I., Dietz S.M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gabart W.M., Glasser K., RA Harris M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M., Howland T.J., Wei M.H., Ibegvam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegvam C., RA Hostin D., Houston K.A., Nixon M.Cheod M.P., Mcherson D., Ketchum K.A., RA Mchallov G., Milshina N.V., Mobarry C., Morris J., Moshreti A., Mohneti A., Murphy B., Murphy L., Wang X., Shih T., Shong W., Zhang G., Zhao Q. Zheng L., Shih H.O., Ra Albance L. Shih R., Shih R., Shang M., Shih H.O., Ra Albance
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Q9VX34;
01-MAY-2000 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
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ATP-binding; Helicase; Hydrolase.
NON TER 745 745
SEQUENCE 745 AA; 85831 MW; F689AC
SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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69 DFSAGLIIGGK 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10731132;
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22,
27,
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Last annotation update)
 Kronmiller B.,
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Pred. No.
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   Carlson J.W., Halpern
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Yao Q.A., Ye J.,
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InterPro; IPR001545; DEAD/DEAH.N.
InterPro; IPR001659; DEAD box.
InterPro; IPR001650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
SMART; SM00487; DEXDC; T.
SMART; SM00490; HELICC; T.
SMART; SM00490; HELICC; T.
PROSITE; PS00039; DEAD ATP HELICASE; UNKNOWN_1.
ATP-binding; Helicase; Hydrolase.
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Hradecky P., Huang Y., Kaminker JS., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Kaminker J.S., Bergman C.M., Kronmiller
Patel S., Frise E., Wheeler D.A., Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003506; AAF48747.2; -. EMBL; AY119628; AAM50282.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celniker S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Base; FBgn0030855; CG5800.
GO:0005524; F:ATP binding; IEA.
GO:0008026; F:ATP-dependent helicase act
GO:0003676; F:nucleic acid binding; IEA.
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me Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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EFGAGLVLGGQ 11 : | | | | : : | | :
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                                                                                                   Pred. No. with the state of the
                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                              92A2897054268066 CRC64;
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, Nelson C.R.,
Sodergren E.J.,
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., Park S.,
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## GO:003724,
## GO:003724,
## GO:0003724,
## GO:0003724,
## InterPro; IPR000629;
## InterPro; IPR000629;
## InterPro; IPR000650; #ell.
## Pfam; PF00270; DEAD; 1.
## DR SMART; SM00490; HELICC; 1.
## SMART; SM00490; HELICC; 1.
## PROSITE; PS00039; DEAD ATP HELICASE; 1.
## PROSITE; PS00039; DEAD ATP HELICASE; 1.
## GO:
## GO
                                                                             Query Match
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Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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MEDLINB=96301396; PubMed=8660968;

REDLINB=96301396; PubMed=8660968;

Saviteky K., Ziv Y., Bar-Shira A., Gila

Uziel T., Sfez S., Nahmias J., Sartiel

Collins F.S., Shiloh Y., Rotman G.;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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15-JUL-1998 (Rel. 36, I
05-JUL-2004 (Rel. 44, I
Probable ATP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB040537; BAB18536.1; -. HSSP; P10081; 1QVA. SWISS-2DPAGE; Q13206; HUMAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A human gene (DDX10) encoding a putative DEAD-box RNA helicase 11072-\sigma23.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=DDX10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11q22-q23
                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:2735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATABASE: NAME=Atlas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infobiogen.fr/services/chromcancer/Genes/DDX10.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
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  Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             DDX10
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Primates;
                     59.7%;
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t RNA helicase DDX10 (DEAD-box protein 10).
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Catarrhini; Hominidae
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                                                                             -> D (in Ref. 2).
-> E (in Ref. 2).
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      Mismatches
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., Eddy R.L.,
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                                       Length 875;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Schibs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Sobs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Sobs R.A.,
RA Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Tones S. T. Marra M. A.
                                                                                                       Query Match
Best Local :
                                                                         Matches
                                                                                                                                                                                                                                       InterPro; IPR001410; DEAD.
InterPro; IPR001410; DEAD/DEAH N.
InterPro; IPR001545; DEAD/DOXT.
InterPro; IPR001629; DEAD DOXT.
InterPro; IPR00150; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00480; HELICG; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
ATP-binding; Helicase_Hydrolase.
NON_TER.
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2003) to the DEAD box helicase family.
I SIMILARITY: Belongs to the DEAD box helicase family.
EMBL; BC049261; AAH49261.1; -.
EMBL; BC049261; AAH49261.1; -.
EMBL; BC049261; Ddx10.
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ddx10 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones S.J., Marra M.A.;
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                                                                  Local Similarity hes 6; Conserv
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1 EFGAGLVLGGQ 11
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                                                                                                                                                                                                              891 AA; 102289 MW; FCCABEEFA9FA5892 CRC64;
                                                                     Conservative
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                                                                                                   59.7%; Score 40; DB 2; 54.5%; Pred. No. 5e+02;
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                                                                  4; Mismatches
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Search completed: December 9, Job time: 9.96223 secs 2004, 09:20:51

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Maximum Match 100%
Listing first 45 summaries
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                     478139 segs, 66318000 residues
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US-09-215-212-12
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US-09-252-991A-18909
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US-09-252-991A-31106
US-09-252-991A-20850
US-09-252-991A-20850
US-09-134-000C-4497
US-09-134-000C-4497
US-09-134-000C-4657
US-09-146-661-2
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US-09-146-661-2
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                                                                                         Sequence 12, Appl Sequence 130, Appl Sequence 18909, A Sequence 27542, A Sequence 24977, A Sequence 33086, A Sequence 31069, A Sequence 31106, A Sequence 31106, A Sequence 31065, A Sequence 31065, A Sequence 30065, A Sequence 2968, Ap Sequence 2968, Ap Sequence 29729, A Sequence 20850, A Sequence 20850, Ap Sequence 20874, A Sequence 20850, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli
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US-09-215-212-13
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Best Local S
Matches 13
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Patent No. 6372207
GENERAL INFORMATION:
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35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35
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US-09-252-991A-27456	US-09-579-174-14	US-09-107-858-14	US-08-758-621-14	US-09-579-174-2	US-09-107-858-2	US-08-758-621-2	US-09-461-436B-52	US-08-513-974B-360	US-08-513-974B-52	US-10-140-002-472	US-07-732-242C-7	US-09-247-155-163	US-09-579-174-23	US-09-579-174-22	US-09-107-858-23	US-09-107-858-22	US-09-621-976-5202
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
27456, A	14, Appl	14, Appl	14, Appl	2, Appli	2, Appli	2, Appli	52, Appl	360, App	52, Appl	472, App	7, Appli	163, App	23, Appl	22, Appl	23, App1	22, App1	5202, Ap

### ALIGNMENTS

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Sequence 13, Application US/09215212
Patent NO. 6372207
GENERAL INFORMATION:
APPLICANT: TEPPER, Mark
APPLICANT: CUNNINGHAM, Mark
APPLICANT: SHERRIS, David
APPLICANT: SHERRIS, David
APPLICANT: MCKENNA, Sean
TITLE OF INVENTION: IFNACYIFN COMPLEX
FILE REFERENCE: TEPPERIA.SEQ
CURRENT APPLICATION NUMBER: US/09/215,212
CURRENT FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TEPPER, Mark
APPLICANT: CUNNINGHAM, Mark
APPLICANT: EL TAYAR, David
APPLICANT: EL TAYAR, Nabil
APPLICANT: EL TAYAR, Nabil
APPLICANT: MCKENNA, Sean
TITLE OF INVENTION. IFMARZ/IEN COMPLEX
FILE REFERENCE: TEPPERIA.SEQ
CURRENT FILING DATE: 1998-12-18
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/68,295
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LEGIH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION. Description of Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: C terminal human ; OTHER INFORMATION: SIFNAR2 linked by linker to N terminal human IFNDeta US-09-215-212-12
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Pred. No. 0.00023;
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US-09-252-991A-18909
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US-09-252-991A-18909
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                                                      PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18909
LENGTH: 360
TYPE: PRT
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Patent No. 6551795
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GENERAL INFORMATION:
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LENGTH: 34
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/068,295
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
ORGANISM: Pseudomonas aeruginosa
                                          ENGTH: 640
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Pred. No. 42;
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Pred. No. 0.00038;
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Query Match
Best Local Similarity
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US-09-252-991A-32724
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                                                                                                                                                                                                   APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46190
LENGTH: 321
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Patent No. 6703491
GENERAL INFORMATION:
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Matches
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196:136
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Best Local
                                                                                                                                                                                         LENGTH: 32
TYPE: PRT
                                                                                                                                     ORGANISM: Drosophila melanogaster FEATURE: OTHER INFORMATION: Xaa means any amino acid
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TYPE: PRT
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 189
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                              1 EFGAGLVLGGO 11
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8; Conserv
DFSAGLIIGGK 199
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                                                             Conservative
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77.8%;
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54.5%;
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80.0%;
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2; Mismatches
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Pred. No. 77;
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Pred. No.
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RESULT 7 US-09-252-991A-24977

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CURRENT PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-19
PRIOR FILING DATE: 1998-07-27
VUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24977
LENGTH: 903
TYPP: """
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US-09-252-991A-23386
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                                  GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
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SEQ ID NO 23386
LENGTH: 494
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GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. SEQ ID NO 33609
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Patent No. 6551795
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Patent No. 6551
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TITLE OF INVENTION:
FILE REFERENCE: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MARC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Local Similarity 64.3%;
les 9; Conservative
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NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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77.8%;
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Pred. No. 2.5e+02;
1; Mismatches 1
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                                                                                                                      ; ORGANISM: Klebsiella
US-09-489-039A-11069
                                                                                                                                                                                                                                                                                                                                                                                       US-09-489-039A-11069
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Best Local S
Matches 6
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SEQ ID NO 7178
LENGTH: 150
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                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 11069 LENGTH: 443
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gary Bro
                                                                                                                                                                                                                                                                                                                                                     Sequence 11069, Application US/09489039A Patent No. 6610836
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Best Local
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Best Local
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CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GARY BRETON
                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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les 6; Conserv
136 FGQGLGLGGEW 146
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                                                        Similarity
7; Conserv
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                                                           Conservative
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Pred. No.
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Pred. No.
                                                            Mismatches
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RESULT 12

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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 33065
LENGTH: 574
TYPE: PRI
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US-09-540-236-2968
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31196
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  Sequence 2968, Application US/09540236
Patent No. 6673910
GENERRAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT ELLING DATE: 2000-04-04
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NUMBER OF SEQ ID NOS: 3840
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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72.7%;
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Pred. No.
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Pred. No.
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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-20850
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US-09-252-991A-20850
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                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELICATION NUMBER: US 60/094,190
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29929
LENGTH: 213
TYPE: PETER DATE: 1998-07-27
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US-09-252-991A-29929
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Best Local :
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LENGTH: 239
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Best Local :
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LENGTH: 153
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                          TYPE: PRT
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ORGANISM: M.catarrhalis
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7; Conserv
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       Conservative
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87.5%;
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   Score 36; DB 4; Le
Pred. No. 2.4e+02;
2; Mismatches 2;
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Pred. No. 2.2e+02;
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Pred. No. 1
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                                       Length 239;
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US-09-252-991A-19484
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US-09-134-000C-4497
                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Enterococcus faecalis US-09-134-000C-4497
                                 Sequence 19484, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin version 3.1 SEQ ID NO 4497 LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SEQ ID NO 26774
LENGTH: 278
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4497, Application US/09134000C Patent No. 6617156 GENERAL INFORMATION:
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                              Local
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ses 7; Conserv
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b. 6551795
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.7%;
87.5%;
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Pred. No. 2.5e
1; Mismatches
                                                                                                                                                                                                                                                                              Score 36; DB 4; I
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                Mismatches
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GAGLVLGG 10

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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-845-295A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08845295A
Patent No. 5817490
 Matches
                Query Match
Best Local (
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Best Local Similarity
                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 60/017
FILING DATE: 17-MAY-1996
ATTORNEY AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION UMBER: 38,346
REFERENCE/DOCKET NUMBER: 7043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                          TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                              MOLECULE TYPE:
                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                     LENGTH: 584 amino
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/845,295A FILING DATE: 25-April-97
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Similarity 7; Conserv
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                                                                                                                         584 amino acids
                                                                                                                                                                          423-229-1239
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzymatic Process for the Manufacture Ascorbic Acid, 2-Keto-L-Gulonic Acid, 2-Keto-L-Gulonic Acid
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77.8%;
                53.7%;
87.5%;
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                Score 36;
Pred. No.
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Pred. No.
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5e+02;
                               Length 584;
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146 GGGLVLGG 153

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RESULT 22
US-09-146-661-2
                                              GENERAL.

APPLICANT: Hudds,
TITLE OF INVENTION: Enzymatic...
TITLE OF INVENTION: Ascorbic Acid,2-Keto-,
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Eastman Chemical Company
PORRESSE: Parx 511
                                                                                                                                                                                                                                                                                                                                 밁
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; MOLECULE TYPE: protein
US-09-140-933-2
                                                                                                                                                                                                   Sequence 2, Application US/09146661
Patent No. 6136575
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.7%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 7043:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
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US-09-140-933-2
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APPLICANT:
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OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/140,
FILING DATE: 27-August-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-MAY-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
NAME: Cheryl J. Tubach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COUNTRY: USA
ZIP: 37662-5075
                                     STREET: P.O. Box 511
CITY: Kingsport
STATE: Tennessee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Eastman Chemical Company
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TITLE OF INVENTION:
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ZIP: 37662-5075
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                                                                                                                                     Enzymatic Process for the Manufacture of Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzymatic Process for the Manufacture of Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gulonic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/09/140,933
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Pred. No. 6.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 584;
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                                                                                                                                        Esters of 2-Keto-L-Gu
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RESULT 23
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APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzyma
TITLE OF INVENTION: Ascorb
TITLE OF INVENTION: 2-Keto
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-146-661-2
                                                                                                                                                                                                                                                                                                       COUNIA...
ZIP: 37662-5075
COMPUTER READABLE FORM:
COMPUTER: 3.5 inch disk
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM COMPAtible
COUNTY OF THE COMPATIBLE
WINDOWS 95
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 7043:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-61189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
          TELEFAX: 4: INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.7%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/9/
FILING DATE: 09-SEP-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

FILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT IMPORMATION:

NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432

TELECOMMUNICATION INFORMATION:

TELEPHONE: 423-229-6189
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879;
FILLING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quence 2, Application US/09150515 tent No. 6271006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P.O. Box 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: 1BM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,661
FILING DATE: 03-Septmeber-98
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. BO
CITY: Kingsport
STATE: Tennesse
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SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzymatic Process for the Manufacture of Ascorbic Acid, 2-Keto-L-Gulonic Acid, an 2-Keto-L-Gulonic Acid
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Pred. No. 6.3e+02;
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Query Match
Best Local Similarity
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                                                                                              ; ORGANISM: Enterococcus faecalis US-09-134-000C-6657
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APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO.
TITLE OF INVENTION: ENTENCOCOCCUS FAECALIS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                             NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6657
LENGTH: 70
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SEQ ID NO 19668
LENGTH: 809
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR TILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15
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Pred. No.
                                                Score 35; DB
Pred. No. 97;
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                                                     Sequence 5202, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
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SOPTWARE: PatentIn version 3.1
SEQ ID NO 5500
LENGTH: 91
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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SEQ ID NO 21582
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Best Local
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PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
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APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
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APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CPDV
CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT FILING DATE: 1998-06-30
FARLIER APPLICATION NUMBER: 08/758,621
FARLIER APPLICATION NUMBER: 08/758,621
FARLIER FILING DATE: 1996-11-27
FORTHARE: Patentin Ver. 2.0
FORTHARE: Patentin Ver. 2.0
FORTHARE: PRT
ORGANISM: Arabidopsis thaliana
US-09-107-858-22
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US-09-107-858-23
; Sequence 23, Applicat:
; Patent No. 6162900
; GENERAL INFORMATION:
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; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5202
; LENGTH: 107
; TYPE: PRT
ORGANISM: Homo sapiens
; ORGANISM: Arabidopsis thaliana US-09-107-858-23
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; NAME/KEY: SIGNAL
; LOCATION: -23..-1
US-09-621-976-5202
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US-09-107-858-22
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                                              CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT FILING DATE: 1998-06-30
EARLIER APPLICATION NUMBER: 08/758,621
EARLIER FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 23
LENGTH: 120
                                                                                                                                                                               APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CPDV
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Patent No. 6162900
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                                     TYPE: PRT
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PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: 08/758,621
PRIOR FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
PRIOR TION TO THE T
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US-09-579-174-23
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Best Local Similarity
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; LENGTH: 120
; TYPE: PRT
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US-09-579-174-22
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                                                                                                                               Matches
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APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CPDV
CURRENT APPLICATION NUMBER: US/09/579,174
CURRENT FILING DATE: 2000-05-25
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Patent No. 6590140
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Matches 6
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PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: 08/758,621
PRIOR FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
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No. 6590140
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TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CPDV
CURRENT APPLICATION NUMBER: US/09/579,174
CURRENT FILING DATE: 2000-05-25
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                                                              FGAGLVLGGQFM 13
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                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                   52.2%;
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••
                                                                                                            Score 35; DB 4; Pred. No. 1.7e+02; 3;
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Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
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                                                                                                                                                                          Length 120
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RESULT 33 US-09-247-155-163

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; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 163
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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US-07-732-242C-7
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FILE REFERENCE: GENSET 021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILLNG DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER APPLICATION NUMBER: 60/080,563
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
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Best Local 9
COUNTRY: USA
ZIP: 10016-2088
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72mb
COMPUTER: IBM PC compatible (NEC PC-9801 RX)
OPERATING SYSTEM: MS DOS
SOFTWARBE: ASCII FORM
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,242C
FILING DATE: 19910718
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPN 2-210178
FILING DATE: 10-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/07732242C Patent No. 5298399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: SIGNAL
LOCATION: -34..-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Uozumi, Takeshi; Masaki, Haruhiko;
APPLICANT: Hidaka, Makoto; Nakamura, Akira;
APPLICANT: Maeda, Michihisa; Yoneta, Yasuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: UNSURE
LOCATION: 81,84,87,131,135,143,156
OTHER INFORMATION: Xaa = any one of the twenty amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Maeda, Michihiba; Yoneta, Yasuo
TITLE OF INVENTION: Gene of Urease
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Frishauf,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 54.5%; tes 6; Conservation
                                                                                                                                                                                                                                                                                                                                              STATE: New York
                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                           600 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                              Frishauf, Holtz, Goodman & Woodward, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 3;
Pred. No. 2.9e+02;
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RESULT 36
US-08-513-974B-52
; Sequence 52, Application US/08513974B
; Patent No. 6114139
                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserve
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Best Local Similarity 8/...
7; Conservative
                                                                                                                                                                                                                              Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 472
LENGTH: 229
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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APPLICANT:
APPLICANT:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/140,002
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: P3330R1C59
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (214) 370-1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                       176 GEGFILGGVFV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 FGÁGTVÍG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472, Application US/10140002
o. 6725730
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                                                                                                                  3 GAGLVLGGQFM 13
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Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                   Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                               Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen, Mary E. Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beresini, Maureen
                                                                                                                                             Conservative
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87.5%;
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Pred. No. 3.3e+02;
                                                                                                                                             Score 35; DB 4;
Pred. No. 3.4e+02;
2; Mismatches 3
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                                                                                                                                                                        Length 229;
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                                                                                                                                               Indels
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GENERAL INFORMATION:

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APPLICANT: HOSUY.,
APPLICANT: Fujii, Ryo
APPLICANT: Fujii, Ryo
APPLICANT: Obtaki, Tetsuya
APPLICANT: Obtaki, Tetsuya
APPLICANT: Obgi, Kazuhiro

ITILE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
ITILE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
US-08-513-974B-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: LIM PC COMPATIBLE
COMPUTER: LIM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PILING DATE: 10-AUG-1995
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
ANALY
                                                                                                                                TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-3

FILING DATE: 28-DEC-1994

PRIOR APPLICATION NUMBER: JP 6-2

APPLICATION NUMBER: JP 6-2

FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION UMBER: JP 6-2

FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-AUG-11
PRIOR APPLICATION DATA:
APPLICATION UNBER: 11
FILING DATE: 16-MAR-12
PRIOR APPLICATION DATA:
APPLICATION UNBER: 11
APPLICATION UNBER: 12
FILING DATE: 20-JAN-15
              TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                        REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45
FIELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-AUG-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                     STRANDEDNESS
                                                                                            LENGTH:
                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 6
FILING DATE: 30-SEP-1994
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ZIP: 02109
                                                                          amino acid
                                                                                                                                                                                                                                                            Resnick, David S.
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                                                                                                252
                                                                                                                                                                           617-523-3400
                                                                                         amino acids
            peptide
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30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 360, Appl
Patent No. 6114139
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-0
FILING DATE: 19-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                           FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 11-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                              FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                              FILING DATE: 30-SEP-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-SEP-
                                                                                                                                                                                                             FILING DATE: 02-NOV-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 20-JAN-1
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                             APPLICATION NUMBER: JP 6
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hosoya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinuma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                             30-SEP-1994
                                                                                                                                                                                                                                                                                                                           20-JAN-1995
                                11-AUG-1945
                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1995
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i, Tetsuya
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JP 6-189272
                                              JP 6-189273
                                                                                              JP 6-189274
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Pred. No. 3.
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US-09-461-436B-52
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Patent No. 6538107
GENERAL INFORMATION:
APPLICANT: Shuji Hinuma
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INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
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                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Ploppy disk
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TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
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ADDRESSEE: Edwards & Angell, LLP
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FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
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                                                                                                                                                  FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: BOSTON
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                                                                                                                APPLICATION NUMBER: 6-270 FILING DATE: 02-NOV-1994
                                                                                                                                                                                                           APPLICATION NUMBER:
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Pred. No. 3.7e+02;
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Query Match
Best Local Similarity
Thes 8; Conserve
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; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-461-436B-52
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US-08-758-621-2
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GENERAL INFORMATION:
                           Query Match
Best Local
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,578
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DCI-099
                                                                                                                                                                                                                                                                                             TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
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MEDLIM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,621
FILING DATE:
FILING DAT
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TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                   TYPE: amino acids
TOPOLOGY: linear
OLECTITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
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NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: <
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Similarity 6; Conserv
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FILING DATE: 11-AUG-1994
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(617)227-5941
FOR SEQ ID NO: 2:
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Conservative
                               52.2%;
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   <u>س</u>
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Score 35; DB 2; Le
Pred. No. 5.1e+02;
3; Mismatches 3;
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                                                              Length 339;
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   Indels
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-716-317-7
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US-08-09-869-7
US-09-016-534-9
US-08-097-869-7
US-09-230-637-45
US-09-230-371A-27
US-09-439-856-6
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5171840-6
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5171840-2
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Sequence 16, Appl Patent No. 5480796
Sequence 1, Appli Patent No. 5171840
Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 45, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 13, Appli
                                                                                                                             Sequence 8, Appli
Sequence 5, Appli
Sequence 5, Appli
Patent No. 5171840
Patent No. 5480796
Sequence 15, Appl
Patent No. 5171840
Patent No. 5480796
Sequence 26, Appl
Sequence 24, Appl
Patent No. 5171840
Patent No. 5480796
Sequence 16, Appl
Patent No. 5480796
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# ALIGNMENTS

US/09313942

APPLICANT: REGENERON PHARMACEUTICALS, INC.
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AN
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 8 ; LENGTH: 592 ; TYPE: PRT ; ORGANISM: HO US-09-313-942-8 Query Match
Best Local Similarity
Matches 377; Conserv CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV Homo PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTIKDDDNILFRDSANATSLPVEFMP VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ---PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD Conservative 67.1%; Score 1921; DB 4 77.1%; Pred. No. 8e-151; tive 22; Mismatches 4 4. 44; Indels 46; AND METHODS Length 592; OF MAKING Gaps 180 120 300 240 60 60 300 240 180 120

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TYPE: amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-08-795-473B-5
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NAME: Davidson, Clifford M.

REGISTRATION NUMBER: 32,728

REFERENCE/DOCKET NUMBER: 963.1007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)-997-1028

TELEFAX: (212)-997-1037

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids

TYPE: amino acids
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                                                                                                                                                                                                                                                                              Query Match 67.0%;
Best Local Similarity 96.5%;
Matches 360; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: MS-DOS EDITOR CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795 FILING DATE: 11-FEB-1997 CLASSIFICATION:
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APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A Pharmaceutical Composition for Treating TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection NUMBER OF SEQUENCES: 10
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T: 1140 Avenue of the Americas
New York
: New York
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PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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                                                                                            CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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Pred. No. 1e-150;
1; Mismatches 4;
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TOPOLOGY:
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                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 360; Conserv
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,473
APPLICATION NUMBER: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
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INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acid
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                              TYPE: amino acid
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CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                       VLRKPAAGSHBSRWAGWGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEEPQLS 120
                                                                                                                    MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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                                                    ULRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPBEPQLS
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1140 Avenue of the Americas
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Nahot, Orit
Blum, Herbert E.
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Pred. No. 1e-150;
1; Mismatches
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;Patent No. 5171840
; APPLICANT: KISHMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN F.
;STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA;
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
RESULT 5
5480796-2
;Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
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                                                             Query Match
Best Local S
Matches 355
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Patent No. 6472179

GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING TITLE OF INVENTION: AND USING FILE REFERENCE: REG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25
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                                                                                                                                                                              NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15
LENGTH: 360
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Best Local Similarity 96.5%;
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FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
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                                                               Local Similarity
nes 355; Conserv
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MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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Pred. No. 3.1e-150;
2; Mismatches 0;
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Pred. No. 1e-150;
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APPLICANT: KISHIMOTO, TADAMITSI
TITLE OF INVENTION: RECEPTOR PF
STIMULATORY PACTOR-2
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/2:
APPLICATION NUMBER: US/07/2:
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5480796-7
; Patent NO. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
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Best Local Similarity
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ECEPTOR PROTEIN FOR HUMAN
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; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo 9
US-09-313-942-26
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US-09-313-942-26
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CURRENT APPLICATION NUMBER: US/09/313,94
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS,
TITLE OF INVENTION: RECEPTOR BASED ANT
TITLE OF INVENTION: AND USING
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/09313942
Patent No. 6472179
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Best Local Similarity
Matches 344; Conserv
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                                                                                                                                               Query Match
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PILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
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nes 331; Conserv
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                                                       MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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Pred. No. 2.4e-139;
2; Mismatches 1;
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TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 1168
TYPE: PRT
ROBANISM: Homo sapiens
RESULT 11
5171840-6
;Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
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US-09-313-942-24
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Best Local Similarity
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Pred. No. 6.2e-139;
1; Mismatches 0;
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Patent No. 5480796

APPLICANT: KISHIMOTO, TADAMITSU

TITLE OF INVENTION: ANTIBODIES AGAINST

FOR HUMAN B CELL STIMULATORY FACTOR-2

NUMBER OF SEQUENCES: 8

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/907,650

FILING DATE: 02-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 298,694

FILING DATE: 19-JAN-1989
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NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/298,694

FILING DATE: 19-JAN-1989
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Best Local Similarity
Matches 322; Conserv
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 322; Conserv
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                                                                                                                                                               MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                   CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
                                                                                                VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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                                CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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                                                                                                                                                                                                                             60.9%; Score 1741; DB 6; 1
100.0%; Pred. No. 2.8e-136;
tive 0; Mismatches 0;
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GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

ITITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAK.

ITITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR PILING DATE: 1999-05-19

PRIOR PILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FRENTSEQ for Windows Version 3.0
                                                                                                                                             RESULT 14
5171840-5
                              PATENT NO. 5171840

APPLICANT: KISHIMOTO, TADAMITSU

TITLE OF INVENTION: RECEPTOR PROTEIN

STIMULATORY PACTOR-2

NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA:
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; ORGANISM: Homo sapiens
US-09-313-942-16
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US-09-313-942-16
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 315
                  APPLICATION NUMBER:
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Local Similarity 99.7%;
nes 312; Conservation
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Pred. No. 1.8e-131;
1; Mismatches 0; Indels
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5480796-5
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APPLICANT: KISHIMOTO, TADAMITSU
ITILE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/07/907,650
                                                                                                                                                                                                                                                                                                                                                  5480796-5
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
SEQ ID NO:5:
LENGTH: 386
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                                                                                                                                                                                                                                                                            Query Match 48.5
Best Local Similarity 73.6
Matches 276; Conservative
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Best Local Similarity
Matches 276; Conserv
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                            179
                                                                                  121 CFRKSPLSNVVCEWGPRSTP--SLTTKAVLLVRKPQNSPAEDFQEPCQYSQESQKFSCQL 178
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AVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTW
                                                        CFRKSPLSNVVC--GPRSTPEWSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQL
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                                                                                                                                                                                                                                                                     48.5%; Score 1389; DB 6; Length 386; 73.6%; Pred. No. 5.9e-107; tive 1; Mismatches 4; Indels 9
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Pred. No. 5.9e-107;
1; Mismatches 4;
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RESULT 16 US-09-043-785-1

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RESULT 17
5171840-11
; Patent No. 5171840
; AEPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
;STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
;SEQ ID NO:11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: CHEBATH, Judith

APPLICANT: HALIMI, Hubert

APPLICANT: REVEL, Michel

ITITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY

FILE REFERENCE: Chebath=1

CURRENT APPLICATION NUMBER: US/09/043,785

CURRENT FILING DATE: 1996-09-02

EARLIER APPLICATION NUMBER: PCT/IL96/00119

EARLIER APPLICATION NUMBER: PCT/S15453

EARLIER APPLICATION NUMBER: 115,453

EARLIER APPLICATION NUMBER: 115,453

EARLIER APPLICATION NUMBER: 115,097

EARLIER APPLICATION NUMBER: 118,097

EARLIER APPLICATION NUMBER: 118,097

EARLIER APPLICATION SUMBER: 118,097
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SEQ ID NO 1
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09043785 Patent No. 6172042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
-09-043-785-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 PPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 -----QDSSSVPLP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFSCQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREPOLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAQEEFGQGEWSEWSPEAMGTPWTESRSPP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLSVTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLSVTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KFSCQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEF 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAQEEFGQGEWSEWSPEAMGTPWTESRSPP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPVPPGEDSKDVAAP 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPV--
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US-08-716-317-7
; Sequence 7, Ap;
; Patent No. 591
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-0CT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
DOT/.TD96/00198
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Best Local Similarity
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APPLICANT: HAMA,
APPLICANT: TOHDA,
                                                                                                                                                                                                 TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 17167/1995
FILING DATE: 03-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PRESERVANCE NUMBER: 10-924-0 PRESERVANCE NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION TITLE OF INVENTION: VECTOR CONTAINING IT NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1755 S.
CITY: ARLINGTON
                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWNSSFYRLRFELRYRAERSKTFTTWYVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGE 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQQLAVPEGDSSFYIVSMCVASSVQLAVPE
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Pred. No. 6e-71;
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                                                                                                         US-08-792-019B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08792019B Patent No. 5741772
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                              Matches 187;
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHANG, MITITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CCOK, ROBERT R.
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/792,019B FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: AMOEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 91320
                                                                                                                       LOCATION:
                                                                                                                                                                  LOCATION:
                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                       ENGTH:
354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 NNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMST
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100.0%; Pr/
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                                         Score 938.5; DB 1;
Pred. No. 5.9e-70;
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Pred. No.
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                                                                                                        Query Match
Best Local Similarity
Matches 187; Conserv
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Patent No. 6054294
                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,6
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 9:
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ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
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                                                                                                                                                                                                        FEATURE:
NAME/KEY:
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LENGTH: 212 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/792,019 FILING DATE: 03-FEB-1997 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy |
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                       FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/988,819 FILING DATE: 12-DEC-1997
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                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                 32.8%;
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                                                                                                                 Score 938.5; DB 3
Pred. No. 5.9e-70;
0; Mismatches 3
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RESULT 21
US-09-016-534-9
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                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                    Matches
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APPLICANT: CHANG, MING-SHI
APPLICANT: ELICOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-4
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/016,534
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ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
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APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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TOPOLOGY: li
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 AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF 201
                    AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
                                                              KEALAENNINLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR 141
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97.9%;
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Pred. No. 5.9e-70;
0; Mismatches 3;
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RESULT 23
US-08-795-473B-6
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US-08-097-869-7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     Matches 187;
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APPLICANT: Todaro, George
APPLICANT: Rose, Timothy
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 07/753
PILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUTABBIGE, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2445
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HYBRID CYTOKINES NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rel-ease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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CLASSIFICATION:
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202 LOSSLRALROM 212
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                                                                  LOSSLRALROM 212
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97.9%;
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Pred. No. 5.9e-70;
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US-09-230-637-45
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                                                                                                                                                                                                                                  RESULT 24
                                                                                                                                                                         Sequence 45, Application US/09230637 Patent No. 6264958
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                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity 97.9%;
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APPLICANT: Galun, Eithan
APPLICANT: Galun, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hegatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
**PROPERCES** DAVIDENCE ADDRESS:
              APPLICANT: Hayward, Gary
APPLICANT: Nicholas, John
APPLICANT: Hardwick, J. Marie
APPLICANT: Reitz, Marvie
APPLICANT: Reitz, Marvie
TITLE OF INVENTION: No. 6264958el Genes of Kaposi's
TITLE OF INVENTION: Associated Herpesvirus
FILE REFERENCE: 1107.78372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/09/230,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 96:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 11-FEB-19:
CLASSIFICATION:
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CTTY: New York
Vow Yor
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TOPOLOGY: unknown
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SOFTWARE: MS-DOS EDITOR
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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11-FEB-1997
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Pred. No. 5.9e-70;
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; SEQ ID NO 27
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Human
US-09-230-371A-27
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PRIOR APPLICATION NUMBER: 60/022
PRIOR FILING DATE: 1996-07-25
PRIOR APPLICATION NUMBER: PCT US
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows VS
SEQ ID NO 45
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Homo sapiens US-09-230-637-45
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US-09-230-371A-27
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Best Local Similarity 97.9
Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09230371A Patent No. 6348586
                                                                                                                                                                       Matches 187;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 199-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 45185-G-PCT-US
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
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APPLICANT: Russo, James J
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
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APPLICANT:
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Pred. No. 5.9e-70;
0; Mismatches 3
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Pred. No. 5.9e-70;
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                                                                                                                                                                                                                                                                                                                     Query Match
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,473
APPLICATION NUMBER: 08/795,473
FILING DATE: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
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APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A Pharmaceutical Composition for Treating TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/439,856 FILING DATE:
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STATE: New York
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LOSSLRALROM 212
                                 LQSSLRALRQM 543
                                                                     AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
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1140 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: (212)-997-1028
(212)-997-1037
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Blum, Herbert E
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Pred. No. 5.9e-70;
0; Mismatches 3
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RESULT 27

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RESULT 28
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APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth HC
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/09/462,941
CURRENT FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
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                                                                                                                                                                                                              SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERFERON-BETA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
SEQ ID NO 13
LENGTH: 212
TYPE: PRT
                                                                                                       Query Match
Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: REVEL, MICHEL; TIOLLAIS, PIERRE TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
                                                                                                                                                                                              LENGTH: 212
                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                     APPLICATION
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 860,883 FILING DATE: 08-MAY-1986
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 449,447 FILING DATE: 12-DEC-1989
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 208,925 FILING DATE: 20-NOV-1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQMLQDMTTHLILRSFKEF 532
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                                                              354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413
413 KEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR 472
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                                                                                                           Conservative
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                                                                                                                                                                                                                                                     NUMBER: 208,925
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97.9%;
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97.9%;
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Pred. No. 5.9e-70;
                                                                                                         Score 938.5; DB 6;
Pred. No. 5.9e-70;
0; Mismatches 3;
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                                                                                                                                        Length 212;
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RESULT 30
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US-08-469-318-145
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/44
APPLICATION NUMBER: 08/44
FILING DATE:
FILING DATE:
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
GTD ANTONNED ACID
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TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
TYPOTATION TO THE PROTECTION OF TH
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GENERAL INFORMATION:
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o. 6022535
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Best Local
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,609A

FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERSNCE/DOCKET NUMBER: C-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-5986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 145, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1; MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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APPLICANT: Olins, Peter O.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 317 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                     240 DPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQH------HCVIHDAWSGLR 287
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32.7%; Score 935; DE
Similarity 63.0%; Pred. No. 2.1e
06; Conservative 17; Mismatches
LEYLONRFESSEEQARAVOMSTKVLIOFLOKKAKNLDAITTPDPTTNASLLTKLOAONOW 516
                                                      ALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVY
                                                                               ALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVY 456
                                                                                                                                                NKDDDNILFRDSANATSLFVEFMFVFFGEDSKDVAAPHRQFLTSSERIDKQIRYILDGIS
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Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
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                                                                                                                          SGGGSNM----APVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIS
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RESULT 31
US-08-446-872A-145
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/446,872A FILING DATE: 06-JUN-1995 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/192,325 FILING DATE: 14-FEB-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
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STREET: F.
TTTY: Chicago
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                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: C-2790/1
                                                                                                                                                                                                                                                                                                                                                        NAME: Bennett, Dennis
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                      STRANDEDNESS
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                           288 HVVQLRAQEEFGQGEWSEWS------PEAMGTPWT-ESRSPPAENEVSTPMQALTT 336
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                                                                                     240 DPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQH------HCVIHDAWSGLR 287
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                                                          DPNNLNSEDMDILMERNLRTPNLLAFVR-AVKHLENASGIEAILRNLQPCLPSATAAPSR
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Paik, Kumnan
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                                                                                                                   Conservative
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Klein, Barbara K.
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Caparon, Maire H.
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63.0%;
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GDWQEFREKLTFYLVTLEQAQEQQYVIEGRISPGGG------
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                                                                                                                                 Score 935; DB 3; Pred. No. 2.1e-69;
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-762-227A-145
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US-08-762-227A-145
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GENERAL INFORMATION:
                                                                                                                                                      INFORMATION FOR SEQ ID NO: 145: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,54
REFERENCE/DOCKET NUMBER: C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
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Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumman
Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/446,872 FILING DATE: 06-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/762,227A FILING DATE: 09-Dec-1996 CLASSIFICATION: <Unknown>
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Corporate Patent Dept.
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                                                                                         STRANDEDNESS:
                                                                                                           TYPE: amino acid
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                                                                   TOPOLOGY:
                                                                                                                                    LENGTH:
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Braford-Goldberg,
Maire H.
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                                                                                                                               317 amino acids
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                                                                                         <Unknown>
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Best Local Similarity
Matches 206; Conserv
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/192325
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01185
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CLASSIFICATION:
                                                                                          288 HVVQLRAQEEFGQGEWSEWS------PEAMGTPWT-ESRSPPAENEVSTPMQALTT 336
                                                                                                                                                                 240 DPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQH------HCVIHDAWSGLR 287
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NKDDDNILFRDSANATSLPVEFMPVPPGEDSKUVAAPHRQPLTSSERIDKQIRYILDGIS
                                                                                                                               DPNNLNSEDMDILMERNLRTPNLLAFVR-AVKHLENASGIEAILRNLQPCLPSATAAPSR
                                                     HPIIIKA-----GDWQEFREKLTFYLVTLEQAQEQQYVIEGRISPGGG------ 125
                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQW 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LODMTTHLILRSFKEFLOSSLRALROM 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQDMTTHLILRSFKEFLQSSLRALRQM 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQW
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-1995
                                                                                                                                                                                                                           32.7%;
63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multivariant IL-3 Hematopoiesis Fusion Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.7%; Score 935; DB 4; Length 317; 63.0%; Pred. No. 2.1e-69; tive 17; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196
                                                                                                                                                                                                          17;
                                                                                                                                                                                                          Score 935; DB 5; Length 317; Pred. No. 2.1e-69; 7; Mismatches 48; Indels
                                                                                                                                                                                                        56;
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                                                                                                                                                                                                        Gaps
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; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-567-047-2
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                                                                            Matches
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US Patent No. 5789552 Patent No. 5789552 5789555
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SAVINO, ROCCO
APPLICANT: LAHM, Armin
APPLICANT: CILIBERTO, Gennaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Policy
                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                               TELEPHONE: 202-0-0
TELEPHONE: 202-0-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 04-DEC CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                360 PVPPGEDSKDVAAPHROPLTSSERIDKOIRYILDGISALRKETCNKSNMCESSKEALAEN 419
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PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                      202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-1995
                                                                         32.6%; Score 934; DB 1; 1 100.0%; Pred. No. 1.1e-69; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/567,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #1.30
                                                                                                              Length 184;
                                                                            Indels
                                                                         Gaps
60
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RESULT 35
US-08-567-048-2
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                                                                                                                                                       Query Match
Best Local S
Matches 184
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APPLICANT: SAVINO,
APPLICANT: LAHM, A-
APPLICANT: CILIBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08567048
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/567,048
FILING DATE: 04-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO=1
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                  TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORN
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540
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                  420 NLNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK
                                                                                                    360 PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN
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                                                                                                                                                          184;
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13
                                                                                                                                                                                                                                                                                           amino acids
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  NLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK 120
                                                                         PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAHM, Armin
CILIBERTO, Gennaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                     32.6%; So ilarity 100.0%; E Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IT RM93A000409
                                                                                                                                                     Score 934; DB 2; ]; Pred. No. 1.1e-69; 0; Mismatches 0;
                                                                                                                                                                                            Length 184
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOR HORMONES HAVING
                                                                                                                                                          0
                                                                                                                                                     Gaps
                                    479
                                                                           60
                                                                                                                   419
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PATENT NO. 5186931

PATENT NO. 5186931

APPLICANT: Kishimoto, Tadamitsu;Hirano, Toshio;Akiyama, Yukio;
Okano, Akira;Matsui, Hiroshi;Takahara, Yoshiyuki

TITLE OF INVENTION: COMPOSITION AND METHOD FOR SUPPORTING BONE
MARROW TRANSPLANTATION

NUMBER OF SEQUENCES: 2

CURRENT APPLICATION NUMBER: US/07/366,866
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US-07-632-070B-1
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/07632070B Patent No. 5264209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Mikayama, Toshihumi
APPLICANT: Kadoya, Toshihiko
APPLICANT: APPLICANT: Kakitani, Makoto
APPLICANT: APPLICANT: Inoue, Hideo
TITLE OF INVENTION: Modified hIL-6
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 81,746
FILING DATE: 05-AUG-1987
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                      STREET: 2
CITY: Chi
                                                                                                 COUNTRY: United States of America
                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, ADDRESSEE: Murray & Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 184
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                                                                                                                    Illinois
                                                                                                                                                           20 South Clark Street,
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                                        5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                             Suite 2100
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US-07-918-181A-2
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                                                     SOFTMARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07918181A Patent No. 5338833
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 2-32
FILING DATE: 13 FEB 1990
APPLICATION NUMBER: JP 2-22
FILING DATE: 22 AUG 90
APPLICATION NUMBER: JP 2-25
APPLICATION NUMBER: JP 2-25
FILING DATE: 21 SEPT 1990
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185
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Matches
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            TELEFAX: 212-64
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF INVENTION: C-Terminal IL-6 Muteins NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: ImClone Systems Incorporated STREET: 180 Varick Street
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
             TELEPHONE: Z12 C TO NO:
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                                                                                                                                                                                                                                                                                                                                      STREET: 180 Va.
CITY: New York
                                                                                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                               COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                           United States
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                                            212-645-1405
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100.0%; Pre
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100.0%; Pred. No. 1.1e-69;
tive 0; Mismatches 0;
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; MOLECULE TYPE: protein US-08-231-575-2
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Query Match 32.6%; Score 934; DB 1; Best Local Similarity 100.0%; Pred. No. 1.1e-69; Matches 184; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-UUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08231575 Patent No. 5565336
                                                                                                                                                                                       TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Fowlker
                                                                                               TYPE: amino acids
TOPOLOGY: 1:-
                                                                                                                                                                                                                                            NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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TITLE OF INVENTION: C-Terminal IL-6 Muteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
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TYPE: ami
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN
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amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: ImClone Systems Incorporated
180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States
                                                                                                                                                                                                                            212-645-1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%; Score 934; DB 1; 100.0%; Pred. No. 1.1e-69; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                 FOW-2
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                                     DB 1; Length 185;
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TOPOLOGY: LINEAR; MOLECULE TYPE: PROTEIN US-08-246-427A-5
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US-08-246-427A-5
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                                                                                                                                                                                                                                                                                       TELEFAX: 201-994-1744
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 AMINO ACIDS
TYPE: AMINO ACID
STRANDENNESS:
                                                                                                                                                 Query Match 32.6%; Score 934; DB 1; Length 185; Best Local Similarity 100.0%; Pred. No. 1.1e-69; Matches 184; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08246427A Patent No. 5641657 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTMARE: WORD PERECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/246,427A

FILING DATE: Submitted herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/246,427

FILING DATE: MAY 19, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-
TELEPHONE: 201-994,1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ROSELAND
STATE: NEW JERSEY
                                                                       182 LRQM 185
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### SUMMARIES

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Human IL-	Soluble h	Amino aci	B cell st	Human int	Human int	Bovine ir	Human int	Human int	Human int	IL8-R typ	Human int	Human cyt	Fusion po	Human cyt	Fusion po	B cell st	SR345 pro	Human int	1

## ALIGNMENTS

#### RESULT 1 AAVO3164 IID AAVO XX AAVO XX AAVO XX AAVO XX SOLU XX SOLU XX SOLU XX Huma XX Chimeric sIL-6R/IL-6 protein. 11-JUN-1999 WO9902552-A2 Synthetic. AAY03164; AAY03164 standard; protein; (first entry) 543 Å

Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6; chimeric protein; fusion protein; cell growth inhibitor; melanoma cell; highly malignant cancer cell; in vivo engraftment; mammalian cancer; human haematopoietic cell; bone marrow transplantation; mammalian cancer; hepatotoxic agent protection; haematopoiesis; liver disorder; neurological disorder.

21-JAN-1999

09-JUL-1998; 98WO-IL000321.

10-JUL-1997; 30-DEC-1997; 97IL-00121284. 97IL-00122818.

(YEDA ) YEDA RES & DEV CO LTD.

Revel M, Chebath J, Lapidot T, Kollet

0

WPI; 1999-120776/10.

New glycosylated soluble IL-6 receptor/IL-6 conjugates - used treating cancers, bone marrow transplantation, increasing haem or treating liver or neurological disorders. used for e.g. haematopoiesis

Claim 6; Fig 3; 77pp; English.

This sequence represents the chimeric glycosylated soluble interleukin-6 receptor (sII-6R)-interleukin-6 (II-6) protein (sII-6R/II-6) of the invention. It comprises a fusion protein product between all of the naturally occurring form of sIL-6R and all of the naturally occurring form of II-6, the sIL-6/II-6 and analogues being glycosylated in a similar fashion to the glycosylation of naturally occurring sII-6R and III-6. The sIL-6/II-6 and analogues are capable of inhibiting the growth of highly malignant cancer cells, e.g. melanoma cells, eliciting the in vivo

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              engraftment of human haematopoietic cells in bone marrow transplantation and protecting liver from hepatotoxic agents. They can be used for the preparation of a medicament for treating mammalian cancers by way of inhibition of cancer cells, for enhancement of bone marrow transplantation by way of eliciting engraftment of human haematopoietic cells in bone marrow transplantation, for increasing haematopoiesis, for treating liver or neurological disorders, or in other applications in which IL-6 or sIL-6R are used
                                                                        Human; interleukin-6; receptor; DS-sII-6R; antibacterial; virucide;
anti-HIV; antirheumatic; antiarthritic; antiinflammatory;
                                                                                                                                                 11-JUN-2003
                                                                                                                                                                                                        ABP72702 standard;
                             Homo sapiens
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                                                        immunosuppressive; gene therapy.
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                                                                                                                 interleukin-6-receptor isoform DS-sIL-6R fusion protein
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Best Local S
Matches 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion protein having a functional IL-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunolo treatment.
                                                                                                                                                                                                                                                                                                                 Sequence 570 AA;
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VPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQ
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                                                                                                                                   VLRKPAAGSHPSRWAGMGRRLLLLRS VQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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                                                                                                                                                                                 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                             CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDDFQEPCQYSQESQ-FSCQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 5; 46pp;
                                                                                                                                                                                                                                                  Conservative
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/label= C-myc tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= IL-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= DS-sIL-6R
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Synthetic.
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The invention relates to the production of a fusion protein comprising the human interleukin 6 receptor (IL-6R) fused to the human IL-6 protein in a Pichia pastoris yeast cell. This sequence represents the IL-6R/IL-6 fusion protein. The coding sequence for this protein is cloned into an expression vector for introduction into P. pastoris. The IL-6R protein is used as a drug for amplifying myeloid stem cells and increasing platelets.
                                                                                                                                                                                                                                                            Yeast of Pichia Pastoris genus transformed by expression vector containing gene encoding fused protein of interleukin-6 receptor (IL-6R) protein for amplifying myeloid stem cells and increasing platelets.
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                                                                                                                                                                                                           Example 1; Page 8-10; 11pp; Japanese
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protein interaction; therapeutic; antagonist.
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                                                                                                                                                                                                                              polypeptide H-IL-6 with 18 amino acid linker
                                                                                   1. .19
/label=
/label= linker region
/note= "Links together COOH-terminus
NH2-terminus of IL-6"
                                                                                                               Location/Qualifiers
                                                         /note=
                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                          entry)
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96.8%;
                                            .341
                                                         "H-IL-6 fusion polypeptide"
                                                                                   signal_peptide
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Pred. No. 6.66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conjugate of two peptide(s) with mutual affinity connected by a linker used to modulate interactions between proteins, e.g. for ex vivo expansion of human stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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hes 509;
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DB; AAT97848.
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LIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRAL
                    LIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRAL
                                                                                                                                          VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEDEDNATVHW
                                                             LNLPKWAEKDGCFQSGFNEETCLVKITTGLLEFEVYLEYLQNRFESSEEQARAVQMSTKV
                                                                                  LNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKV
                                                                                                                       VPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENN
                                                                                                                                                                                    GEWSEWSPEAMGTPWTESRSPPARGGGGS------
                                                                                                                                                                                                                 GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                                                                                                                                                                                                                                             PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                                                                                                                                  PHSWNSSFYRLRFELRYRAERSKTFTTWWVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
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                                                                                                                                                                                                                                                                                                                                                                                                 CFRKSPLSNVVCEWGPRSTPSLITKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                   VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEBPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPOLS
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                                                                                                                                                                                                                                                                                                                                                                        CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.5%;
93.7%;
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Pred. No. 1e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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489;

Conservative

Indels

43;

Gaps

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Similarity

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MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

60

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RESULT 5
AAW36847
ID AAW3
XX AAW3
AX AAW3
AX 25-M
DT 25-M
AX 25-M
DT 25-M
AX Inte
XX Inte
XX Inte
XX Inte
XX Prot
OS Synt
OX Prot
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    Query Match
Best Local S
Matches 489
                                                                                    This sequence represents the fusion polypeptide H-IL-6 which contain 13 amino acid linker which joins the carboxy terminus of human interleukin-6 receptor (IL-6R) with the amino terminus of human interleukin-6 (IL-6). Such conjugates could be used to modulate interactions between proteins, particularly to overcome interrupted interactions caused by an incomplete interleukin-6 (IL-6) receptor. constructs derived from IL-6 and its receptor, can also be used for vivo expansion of human stem cells, and as a therapeutic IL-6 recept antagonist. (Updated on 25-MAR-2003 to correct PI field.)
                                                           Sequence
                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                            Conjugate of two peptide(s) with mutual affinity connected by a linker - used to modulate interactions between proteins, e.g. for ex vivo
                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                   Rosejohn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein interaction; therapeutic; antagonist
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25-MAR-1998
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DB; AAT97849.
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                                                                                                                                                                                                                                                                               of human
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Links together
NH2-terminus of IL-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= signal_peptide
                                                                                                                                                                                                                                                                               stem
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               87.8%;
90.1%;
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                                                                                                                                                                                                                                                                               cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linker region
                                                                                                                                                                                                                                                  German.
Score 2512.5; DB 2; Pred. No. 8.3e-160; 1; Mismatches 10;
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RESULT 6
AAX30938
ID AAX3
XX AX30938
AC AAX3
XX 19-0
XX IL-6
XW IL-6
KW Stem
XX Homo
OS Synt
XX Synt
XX PF Rey
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New interleukin-6 receptor-interleukin-6 fused protein for growth of bone marrow stem cells and platelets.
                                              WPI; 1999-496648/42.
N-PSDB; AAZ09202.
                                                                                                                                                                                                                         JP11196867-A
                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                 IL-6; interleukin-6; receptor; human; fusion protein;
stem cell; platelet; reduced antigenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY30938 standard;
                                                                                                                          09-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKPQNSPAEDFQEPCQYSQESQKFSCQLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKV
                                                                                                                                                                                                                                                                                                                                                                                                                 receptor/IL-6 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                              CORP
                                                                                                                            98JP-00002921
                                                                                                                                                            98JP-00002921
                                                                                                                                                                                                                                                     Location/Qualifiers
1. .420
/note= "No start co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 419
                                                                                                                                                                                                                                                       "No start codon given"
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Best Local Simi
Matches 410;
                                                                                                                                                          gp130; cytokine antagonist; interleukin; gamma-interferon;
granulocyte macrophage colony-stimulating factor; J peptid
                                                                                                                                                                                                                                                                                                     AAW70797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 419 AA;
                                                                                                             Synthetic.
                                                                                                                                                                                                        Human interleukin-6R-alpha-Fc.
                                                                                                                                                                                                                                        03-FEB-1999
                                                                                                                                                                                                                                                                       AAW70797;
                Peptide
                                                Protein
                                                                                            Homo sapiens
                                                                                                                                        transforming growth
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                                                                                                                                                                                                                                      (first
              /note= "human IL-R-alpha"
1. .19
/note= "signal peptide"
                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     1 419
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                                                                                                                                           factor-beta.
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This invention describes a novel gene which encodes a fusion protein of interleukin-6 (II-6) receptor and bound with a gene sequence encoding for II-6 at the downstream of II-6 receptor gene. The gene and its encoding protein has applications for the growth of bone marrow stem cells and platelets. Transmission of a signal of II-6 to target cells for stimulation with reduced antigenicity is possible. This sequence represents the II-6 receptor/II-6 fusion protein described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 5-8; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPQLSCFRKSFLSNVVCEWGFRSTFSLTTKAVLLVRKFQNSFAEDFQEFCQYSQESQKFS
MSTKVLIQFLQKKPKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKDFLQS
                            MSTKVLIQFLQKKAKNLDAITTPDPTTINASLLTKLQAQNQWLQDMTTHLILRSFKEFLQS
                                                                                                        LAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLDFEVYLEYLQNRFESSEEQARAVQ
                                                                                                                                     LAENNLNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQ
                                                                                                                                                                                                                    ---APVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEA
                                                                                                                                                                                                                                                      VEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEA
                                                                                                                                                                                                                                                                                                                                                                  EEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPOLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFS
                                                                                                                                                                                                                                                                                                                                EEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILSSELV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      VTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.1%;
95.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2149.5; DB 2
Pred. No. 1.4e-135;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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Best Local S
Matches 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the amino acid sequence of human interleukin (II)-6R-alpha-Fc. The protein is used in the course of the invention. The specification describes cytokine antagonists comprising only the extracellular domain of the specificity-determining component of the cytokine receptor and the extracellular domain of a signal-transducing component of the cytokine receptor. The cytokine is an interleukin (II-1, II-2, II-3, II-4, II-5 or II-15), granulocyte macrophage colony-stimulating factor (GW-CSF), gamma-interferon or transforming growth factor-beta (TGP-beta). The antagonist is capable of transforming growth factor-beta (TGP-beta). The antagonist is capable of binding the cytokine to form a nonfunctional complex. The compounds have therapeutic activity as cytokine antagonists and can also be used in assays for identifying novel agonists and antagonists of cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine antagonists - comprising (determining and signal-transducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                 WVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                             MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 AA
                                                                                                                                                                                                                                                                                            VLRKPAAGSHPSRWAGWGRRLLILRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                  CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                         VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                       GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                                                                                              PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                      PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                       PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
      VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETÇNKSNMCE--SSKEALAE
                                                                                                              PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                     GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ---
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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371. .:
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                                                                                                                                                                                                                                                                                                                                                                                                            67.1%; Score 1921; DB 2; 77.1%; Pred. No. 4.2e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "changed to accomodate a Kozak sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising extracellular domains of specificity-transducing components of cytokine receptor.
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The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (gR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (gR-alpha; beta-1) that act as antagonist to the cytokine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
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19-MAY-1999;
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                                                                                                                                                                                                                                                                                         form
                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule for treating cytokine-related diseases disorders encodes a fusion polypeptide capable of binding a cytokine to
                                                                                                                                                                                                                                                                                                                                                                                                                                  Stahl N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1999;
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99US-00313942.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC binding the cytokien to form a non-functional complex. The receptor CC components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the CC factor) family of cytokines. The invention provides the basis for the CC development of IL-6 antagonists, as they show that if, in the presence of CC ligand, it salpha recepotr and its beta-1 receptor component, can be CC formed, it will effectively block the action of the ligand. Effective consists of the extracellular CC domains of the alpha specificity determining components of their CC receptors and the extracellular domains of the alpha specificity determining components of their CC inaccessbile to form a signal transducing component the native CC membrane-bound forms of their receptor. The nucleic acids and CC polypeptides are useful for treating cytokine-related diseases or CC disorders such as osteoporosis and primary and secondary effects of CC cancer including multiple myeloma or cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
          Cytokine; cytokine-related disease; immunomodulator; osteoporosis; cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; human.
                                              Human IL-6Ralpha-Fc
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                                                                                                                                                                                 STYRVVSVL
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Pred. No. 4.2e-120;
2; Mismatches 44;
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22-MAR-2001;
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(YANC/)
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 GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ---
                                                                                                                                                                                                                                                                                          Conservative
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2001US-00787835.
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The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors for treating cytokine-related diseases or disorders e.g. cancer, cachexia, arthritis and osteoporosis. The present sequence is human I
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                                                                                                                                                                                                                                                                                                                                                   CFRKSPLSNVVCEWGPRSTPSLTTKÄVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ULRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                            PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                  PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                                                                                           PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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359. .360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Inter-chain disulphide bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.1%; Score 1921; DB 7; 77.1%; Pred. No. 4.2e-120; tive 22; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Ala-Gly bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 46;
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RESULT 10
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                   8
                                                                Query Match
Best Local S
Matches 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-1988;
25-JAN-1988;
04-AUG-1988;
14-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP325474-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B cell; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of a re (BSF2 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
31-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP90284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                  Receptor protein for human B cell stimulating factor-2 - obtd. recombinant DNA techniques and used as diagnostic prophylactic therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-1989
                                                                                                                                                                                         The cDNA in AAN90340 was derived from monocyte cell line U937. Isolated BSF2 receptor and DNA encoding it are claimed, as are (b) expression vectors; (c) host organisms; (d) antibodies; and (e) hybridomas. (Update on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                   Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kishimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KISH/) KISHIMOTO
                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1989-214667/30
                                                                  360;
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                                                                                      Similarity
                                                                                                                                                                                                                                                                                            Page 19-21; 63pp; English.
                                                                                                                                                      468
MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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(first ent
                                                                    Conservative
                                                                                                                                                      AA;
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88JP-00012599.
88JP-00194885.
89JP-00007461.
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/label= hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= hydrophobic 362. .386
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                                                                                      67.0%;
96.5%;
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                                                                      Score 1918; DB 1
Pred. No. 5e-120;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for human B
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                                                                                                                DB 1;
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                                                                                                              Length 468;
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(Updated
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RESULT 11
AAR37215
ID AAR377215
AC AAR37
XX Inter
DT 13-SI
XX Inter
CX IT-6
XX Inter
CX IT-6
XX Inter
CX IT-6
XX IT-7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncat transmembrane; multiple myeloma; binding; ability; signal transfer; disease; intracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR37215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR37215;
                                                                                               This sequence represents an interleukin-6 (IL-6) receptor. Varien the receptor lacking either the immunoglobulin-like domain or the transmembrane and intracellular domain have IL-6 binding ability signal transfer ability. Either the full length or truncated IL-6 signal transfer ability. Either the full length or truncated IL-6 receptors may be used for diseases caused by IL-6 such as multiply
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP05091892-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1993
                                                                                                                                                                                                                                                                               New interleukin-6 receptor deriv.
e.g. multiple myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-1991;
                                                                                                                                                                                                                                      Disclosure; Page 10-12;
                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                    (KISH/) KISHIMOTO C.
(CHUS ) CHUGAI PHARM
(TOYJ ) TOSOH CORP.
                                 Sequence
                                                                                myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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67.0%;
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The present invention describes a composition (I) comprising a recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The DCRS2 polypeptide is useful for binding ligands and for preparing antibodies. The DCRS2 polypeptide is also useful for modulating cell proliferation, for diagnostic and therapeutic applications, for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36655
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                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation; apoptosis; erythropoiesis; peripheral arterial disease; cancer; ischaemia; coronary arterial disease; inflammatory condition; rheumatoid arthritis; reperfusion injury; neonatal stress; infection; stroke; preeclampsia; atherosclerosis; cystic fibrosis; wound healing
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Pred. No. 5e-120;
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Best Local
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N-PSDB; AAD45938.
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Human; interleukin-6; IL-6 receptor alpha; IL-^R alpha; IL-6; hepatocyte;
                                  Amino acid sequence of human interleukin-6 (IL-6) receptor alpha.
                                                                    05-NOV-2002
                                                                                                                                   ABB78191 standard; protein;
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Pred. No. 5e-120;
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Matches 360; Conserv
                                                                                                                                                                                                                                                                                                                                                                     GR molecule. Administration of the fusion protein results in the increased expression of one or more of MIP-lalpha, MIP-lbeta, RANTES or IP-10. Also claimed are a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disorder or an immunological disorder (especially rheumatoid arthritis), when it is desirable to increase or resolve an immune response (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the protein sequence of the human interleukin-6 receptor (IL-6R). A soluble receptor is obtained either through proteolytic cleavage or differential mRNA splicing splicing of IL-6R (see ABP72698). The present invention relates to a fusion protein (see ABP72702) comprising a functional IL-6 molecule and a functional DS-sIL-ABP72702)
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 46pp; English.
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antirheumatic; antiarthritic; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP72697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003014359-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein having a functional IL-6 and DS-sIL-6R molecule, ful for the manufacture of a medicament for the prophylaxis or atment of an infectious disease, and an inflammatory or immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
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   61
                                                                                                                                                                                                                                                                                                                    468
                                                                                                 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
   VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----QDSSSVPLP 365
                                                             MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Topley N;
                                                                                                                                                                                         Conservative
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96.5%;
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                                                                                                                                                                               Score 1918; DB 6
Pred. No. 5e-120;
1; Mismatches
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                                                                                                                                                                                      4; Indels .
                                                                                                                                                                                                                                                Length 468;
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                                                                                                                                                                                         Gaps
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RESULT 16
ADC07187
ID ADC077
XX ADC077
XC ADC0
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                                                                                                                                                                                                                                                            Composition potentially useful for treating immunological disorders, comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNAX cytokine receptor subunit 2; DCRS2; cell physiology; cell development; cell culture; interferon detection; immune system disorder; interleukin 6; IL-6; receptor subunit alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1999; 99US-0137159P.
31-MAY-2000; 2000US-00588113.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Dowling
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                                                                                                                                                                                                                                                                                                                                                                          2003-730048/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KASTELEIN R A.
BAZAN J F.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gorman DM,
                                                                                                                                                                                                                                                                                                                                                                                                                              Kastelein RA,
                                                                                                                                                                                                                                                                                                                                                                                                                              Bazan
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The invention describes a composition of matter (1) comprising a substantially pure or recombinant DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein comprising a DCRS2 sequence. A composition of matter comprises: a substantially pure or recombinant DCRS2 polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids

Disclosure;

SEQ

ID NO 12; 41pp; English.

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RESULT 17
AAY92195
ID AAY92195
AC AAY92
XX AAY92
XX II-AH
DT 01-AH
XX II-6H
KW II-6H
KW FUSIC
XX Synth
OS Synth
OS Homo
XX Homo
XX Homo
XX PT Prote
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 468
                                                                                                                                                                                                                                                                                                                                                  AAY92195 standard; protein; 690
                                  Protein
                                                                Peptide
                                                                                                  Protein
                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                 IL-6R-alpha-C-gamma-1;
                                                                                                                                                                                                                                                  Human IL-6R-alpha-C-gamma-1 fusion protein.
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                                                                                                                                                                                                  protein;
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                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     QDSSSVPLP
                                                                                                                                                                                                  nmma-1; cytokine; antagonist;
cytostatic; immunomodulator;
                                                                       /label= IL-6R-alpha
                                                                                                                  Location/Qualifiers
                                                note= "Ala-Gly bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.0%;
96.5%;
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                   C-gamma-4
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Pred. No. 5e-120;
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                                                                                                                                                                                                    CNTF; receptor;
osteopathic.
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The invention concerns production of antagonists to any cytokine that cutilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta calphal transducing component causing beta-receptor dimerization, the cytokine alpha specificity determining component of the receptor (sr-calpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form components are shared by cytokines such as antagonist to the cytokine by cytokines to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic development of II-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the cytokine component formed, it will effectively block the action of the ligand, its alpha recepotr and its beta-1 receptor component, can be consists of the alpha specificity determining components of the extracellular domains of the ligand. Effectivel components of the extracellular domains of specificity determining components of the cytokine inaccessibile to form a signal transducing components of the resultant component are useful for treating cytokine-related diseases or consorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule for treating cytokine-related diseases disorders encodes a fusion polypeptide capable of binding a cytokine t form a nonfunctional complex.
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19-MAY-1999;
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                                                             Sequence 690 AA;
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Score 1917; DB 3;
Pred. No. 9.4e-120;
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                                                                                                                                                                                              VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                     MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                  PHSWNGSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ 300
                                                                            PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                     CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                      CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sR-alpha) and the extracellular domain of the first beta signal transdu
                                                                     The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta
                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule for treating cytokine-related diseases disorders encodes a fusion polypeptide capable of binding a cytokine of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-1998;
19-MAY-1999;
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fusion protein; cytostatic; immunomodulator;
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                                                                                                                                                                                                                                                           nonfunctional complex.
                                                                                                                                                                                                     4; Page; 152pp; English.
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99US-00313942.
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signal transducing
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28-NOV-1996

(first receptor

Homo sapiens.

rheumatoid arthritis; endotoxic

Interleukin-6; IL; Interleukin-6

L; receptor; antisense oligonucleotide; inhibition; kidney tumour; myeloma; Kaposi's sarcoma; psoriasi

psoriasis;

expression;

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AAR98364
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Best Local Simi
Matches 373;
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                                                                                                                                                                                                         AAR98364 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEEPQLS
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                                                                                                                                                                                                                                                                                                  --YPREAKVOWKVDNALOSGNSOES 416
                                                                                                                                                                                                                                                                                                                                                                                                                                     GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ---
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                                                                                                                                                                                                                                                                                                                                  LNLPKMA----EKDGCFQSGFNEET 441
                                                                                                                                                                                                                                                                                                                                                                                                   VPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENN
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83.8%;
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Pred. No. 7.3e-1
1; Mismatches
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RESULT 20
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AC ABP72
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Matches 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotides may be used to inhibit the expression of the interleukin-6 receptor. Inhibition of expression of the II-6 receptor it useful in the treatment of kidney tumours, myeloma, Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotoxic shock. The antisense oligonucleotides are administered at a dosage of 0.1-100mg/kg, pref. O.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-sense oligo:nucleotide inhibitor against human IL-6R expression for treatment of e.g. tumours, cancers, rheumatoid arthritis, psorias endo:toxic shock, etc.
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18-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                         ABP72699
              11-JUN-2003
                                   ABP72699;
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DB; AAT31441.
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                                                                                                                                                            GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPV----
                                                                                                                                                                         VPPGEDSKDVAAP 373
                                                                                                                                                                                                        PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                          standard;
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95JP-00210739.
              (first entry)
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                                                         protein;
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96.2%;
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Pred. No. 7.9e-120;
2; Mismatches 4;
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GEWSEWSPEAMGTPWTESRSDPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVE 357

GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ

PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ

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PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion protein having a functional IL-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunolog disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; interleukin-6; receptor; PC-sIL-6R; antibacterial;
anti-HIV; antirheumatic; antiarthritic; antiinflammatory;
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                                                                                                                                                                                                                                                                                 Sequence 357 AA;
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                                                                                                                                                                                         1 MLAVGCALLAALLAADGAALAPRRCDAQEVARGVLTSLDGDSVTLTCDGVEDEDNATVHW
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                                                                                                                                                                                                                                            Similarity
                                                                                                                 VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEBPQLS
                                                                                                                                 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                         CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                         PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                      PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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99.7%;
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Pred. No. 7.7e-120;
1; Mismatches 0;
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RESULT 21
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AC AAY92
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IL-6R
KW ILL-6R
KW ILL-6R
KW FUBic
OS Synth
OS Homo
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VO20C
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                                                                                                                                                                                                                                                                                   The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined CC with the cytokine, binds to a first beta signal transducing component to CC form a non-functional intermediate which then binds to a second beta CC signal transducing component causing beta-receptor dimerization, the Soluble alpha specificity determining component of the receptor (SR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form CC components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The inventional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The inventional provides the basis for the CR algand, a non-functional intermediate complex, consisting of the ligand, its alpha recepotr and its beta-1 receptor component, can be CR formed, it will effectively block the action of the ligand. Effective antagonists of the stracellular components of the extracellular domains of the alpha specificity determining components of the extracellular ceptors and the extracellular domain of gpl30. The resultant component bound forms of their receptor. The nucleic acids and CC membrane-bound forms of their receptor. The nucleic acids and conserving multiple myeloma or cachexia
                                                                                                                      Query Match
Best Local S
Matches 375
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                                                                                                                                                                                                                                          Sequence 477
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19-MAY-1999;
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fusion protein; cytostatic; immunomodulator; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                      11 Similarity
375; Conser
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                            MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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                                                                                                                   Score 1912; DB 3;
Pred. No. 1.3e-119;
3; Mismatches 25;
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                                                                                                                                                                             Length 477;
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RESULT 22
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                 The present sequence represents the amino acid sequence of interleukin (IL)-6R-alpha domain. The protein is used in the course of the inventic The specification describes cytokine antagonists component of the extracellular domain of the specificity-determining component of the extracellular domain and the specificity-determining component of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW70804 standard;
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                                                                                                                                                                                                                       Cytokine antagonists - comprising edetermining and signal-transducing
                                                                                                                                                                                                                                                                                                          WPI; 1999-044669/04.
                                                                                                                                                                                                                                                                                                                                                          Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 (REGE-) REGENERON PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFRKSPLSNVVCEWGPRSTPSLITKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
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                                                                                                                                                                15; 46pp; English.
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                                                                                                                                                                                                                       comprising extracellular domains of specificity-transducing components of cytokine receptor.
                                                                                                                                                                                                                                                                                                                                                             Economides A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin (IL)-6R-alpha domain.
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cytokine receptor and the extracellular domain of a signal-transducing

the invention.

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RESULT 23
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Best Local S
Matches 355
                         Isolated nucleic acid molecule for treating cytokine-related diseases disorders encodes a fusion polypeptide capable of binding a cytokine t form a nonfunctional complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soluble IL-6-R-alpha; cytokine; antagonist; CNTF; receptor; fusion protein; cytostatic; immunomodulator; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                component of the cytokine receptor. The cytokine is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or II-15), granulocyte macrophage colony-stimulating factor (GM-CSF), gamma-interferon or transforming growth factor-beta (TGF-beta). The antagonist is capable of binding the cytokine to form a nonfunctional complex. The compounds have therapeutic activity as cytokine antagonists and can also be used in assays for identifying novel agonists and antagonists of cytokines
                                                                                                                                                                                                                                                                                                  25-SEP-1998;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soluble human IL-6-R-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-2000
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                                                                                                                                     WPI; 2000-293165/25
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99US-00313942.
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Example 4; Fig 15; 152pp; English
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The invention concerns production of antagonists to any cytokine that cutilizes an alpha specificity determining component, which when combined component productions of the cytokine beta signal transducing component to component to component a non-functional intermediate which then binds to a second beta component transducing component causing beta-receptor dimerization, the component of the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form component of the cytokine receptor (beta-1) are combined to form component of the cytokine by chinding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the cytokine of II-6 antagonists, as they show that if, in the presence of component, it will effectively block the action of the ligand. Effective components of the extracellular domain of gpl30. The resultant components of the alpha specificity determining components of the extracellular domain of gpl30. The resultant componers, function as high-affinity traps, rendering the cytokine components are useful for treating cytokine-related diseases or component such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia

Sequence 360 AA;

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Cytokine; cytokine-related disease; immunomodulator; osteoporosis; cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; hum

therapy; human.

Human IL-6Ralpha-domain protein

12-FEB-2004

(first

entry)

ABW02172 standard; protein; 360

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RESULT 25
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors an for treating cytokine-related diseases or disorders e.g. cancer, cachesia, arthritis and osteoporosis. The present sequence is human IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding fusion polypeptides capable of binding a cytokine to form a non-functional complex, useful for treating cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
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22-MAR-2001; 2001US-00787835.
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Pred. No. 1.2e-119;
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AAP90525

AAP90525 standard; protein; 468 AA

RESULT 26 ABP72698 ID ABP7

ABP72698 standard; protein; 364

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23-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor protein for human B cell stimulatory factor-2 - used developing prophylactic, therapeutic and diagnostic agents for disorders.
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N-PSDB; AAP90525.
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                                                                                                                                                                                                                                                                                    1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                       VLRKPAAGSHPSRWAGMCRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                         VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAERPAGTVHLLVDVPPEEPQLS
                                              GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                                                                                         PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                         PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                           CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                          CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                         MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVBPEDNATVHW
       VPPGEDSKDVAAP 373
                                                                             PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEBFGQ
                                                                                                                         PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                               GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPV----
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                                                                                                                                                                                                                                                                                                                       Score 1910; DB 1;
Pred. No. 1.7e-119;
1; Mismatches 5;
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differential mRNA splicing. The invention relates to a fusion protein (see ABP72702) comprising a functional II-6 molecule and a functional DS-SIL-6R molecule. Administration of the fusion protein results in the increased expression of one or more of MIP-labeta, MIP-labeta, RANTES or IP-10. High levels of MIP-labha, MIP-labeta and RANTES complete with HIV for binding to CCR5 and effectively suppress HIV entry. The fusion protein can be used in the treatment of any disease in which the invention also provides a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disease or resolve an immune response (claimed) when it is desirable to increase or resolve an immune response (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion protein having a functional IL-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunological treatment of an infectious disease, and an inflammatory or immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; interleukin-6; receptor; DS-sIL-6R; antibacterial; virucide; anti-HIV; antirheumatic; antiarthritic; antiinflammatory; immunosuppressive; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2002; 2002WO-GB003581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soluble interleukin-6 receptor isoform DS-sIL-6R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of a soluble form of the human interleukin-6 receptor (IL-6R), denoted DS-sIL-6R, produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 46pp; English
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                                                                                                                   CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
                                                                                                                                                                                                          VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                               VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                 CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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RESULT 27
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                                                                                                                                                                                                                                                                                                                                  This is a previously reported amino acid sequence for human interleukin-6 (C (hIL-6) receptor alpha. The invention relates to the finding that hIL-6 c is essential for hepatitis B virus (HBV) infection. The invention CC is essential for hepatitisal composition for the treatment of HBV infection, comprising a soluble active agent that interacts with at least one of the binding sites between hIL-6 and the pSI region of HBV and between hIL-6 and hepatocytes and other HBV-permissive cells. The active agent competitively binds to at least one of these sites and thereby prevents thIL-6-mediated HBV infection of hepatocytes and other HBV-permissive cells. The soluble active agent is selected from glycoprotein 80 (gy80) having receptor sites which interact with hIL-6, bill-6 derived competide Gln53-His165, a combined 1 and 2 hIL-6 mutant (mhIL-6 1+2), and mill-6 legislituted with Phel71 to Leu and Ser177 to Arg, and mixtures
                                                                                                                                                  Query Match
Best Local (
                                                                                                                        Matches
                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which prevents interaction interleukin 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment of hepatitis B virus infection - using a soluble active agent which prevents interaction of HBV with hepatocytes mediated by human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-6 receptor; human; hepatitis B virus; HBV; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-1999
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                                                                                                                                                                                                                                                                                                              of any of these
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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                             1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                    468 AA;
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MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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                                                                                                                                                  66.4%;
95.4%;
                                                                                                                                                  Score 1900; DB 2
Pred. No. 8e-119;
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RESULT 28
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This sequence represents the SR345 protein. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is
                                                                                                                                                                                                                                                                                                                                                          Efficient and selective isolation of a gene encoding membrane puwith low or no antigenic binding activity, for diagnosis, study production of drugs treating abnormal functions of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; SR345 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsuchiya M,
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98JP-00279876.
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Best Local S
Matches 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised antibody is carried in a fused protein
AAP90528
                          AAP90528 standard;
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                                                                                                                                                                                                                                                                                                                                                                                     MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 AA;
                                                                                                                                                                                                                    PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                                VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                     GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILF 345
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                                                                                             GEWSEWSPEAMGTPWTESRSPPAENEVSTPMOALTTNKDDDNILF
                                                                                                                                                PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                         protein;
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100.0%; Pr.
0;
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Pred. No. 3.6e-116;
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RESULT 29
AAP90528
ID AAP90528
AC AAP90
XX AAP90
XX AAP90
XX AAP90
XX B cel
XX B cel
XX B cel
XX Homo
XX Clair
                                                                                                                                                                                                                                                                                                  AU8928720-A
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25-JAN-1990
                                                                                                                                                                                                                                              23-JAN-1989;
                                                                                                                                                                                                                                                                        27-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                               cell stimulating factor-2 receptor
                                                                                                                                                                                                                                                                                                                                                     cell stimulating
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                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first en
                                                                                                                                                                                                                                              89AU-00028720
                                                                                                                                                                                                                                                                                                                                                     factor-2 receptor; monocyte U937
                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                        cell
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Receptor protein for human B cell stimulatory factor-2 - used developing prophylactic, therapeutic and diagnostic agents for disorders. for associated

N-PSDB; AAP90525.

14-JAN-1989;

89JP-00007461

(KISH/) KISHIMOTO T.

Claim Page 40; English

The BSF2 receptor has amino acids at the C-terminal deleted. The receptor is derived from a monocyte U937 cell line. It can be used to develop prophylactic and therapeutic pharmaceuticals, as agents to relate diseases and disorders to abnormal BSF-2 prodn. It can also be used to

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RESULT 30
AAY92205
ID AAY92205
XX AAY92207
XX PUSI
DT 01-AI
XX IL-6
XXW Cytc
XXX Synt
OS Synt
OS Synt
OS Hom
XXX Hom
XXX PR
PN WO2
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PN WO2
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(Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL-6 trap; cytokine; antagonist; CNTF; receptor; fusion protein; cytostatic; immunomodulator; osteonathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion polypeptide 616, IL-6 trap
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                                                                                                                    Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to
                                                                                                                                                                                                                                                            Stahl N,
                                                                                                                                                                                                                                                                                                                                                      25-SEP-1998;
19-MAY-1999;
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DB; AAA09047.
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99US-00313942.
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100.0%;
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Pred. No. 9e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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This sequence shows fusion polypeptide

616, which

**2**.

capable of binding

US2003143697-A1 Homo sapiens

Example 6; Fig 25A-F; 152pp; English.

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cc cytokine II-6 to form a non-functional complex. The invention concerns cc production of antagonists to any cytokine that utilizes an alpha cc production of antagonists to any cytokine when combined with the cytokine, combined to a first beta signal transducing component to form a non-cc functional intermediate which then binds to a second beta signal cc alpha specificity determining component of the receptor (s. Falpha) and cc alpha specifically are demain of the first beta signal transducing component combined to form heterodimers (s. cc alpha; beta-1) that act as antagonist to the cytokine by binding the cytokine by cytokine to form a non-functional complex. The receptor components are cytokines. The invention provides the basis for the development of II-c fattagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha cc functional intermediate complex, consisting of the ligand, its alpha cc fectively block the action of the ligand. Effective antagonists of the action of the ligand. Effective antagonists of the extracellular domains of the apphance of correct it will consist of heterodimers of the extracellular domains of the alpha corrections of the cytokine in accessibile to form a signal correction of the intermediate complex with the native membrane-bound forms of their corporations and the cytokine-related diseases or disorders such as osteoporosis and primary corporations and secondary effects of cancer including multiple myeloma or cachexia corporations and primary corporations.
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Best Local
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                                                                                                                                                       Cytokine; cytokine-related disease;
                                                                                                                                                                                                                         Human cytokine trap-616 protein.
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                                                                                                                                cachexia;
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                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                             a-related disease; immunomodulator; osteoporosis;
arthritis; cytostatic; osteopathic; therapy; hum
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Pred. No. 7.8e-111;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors for treating cytokine-related diseases or disorders e.g. cancer, cachexia, arthritis and osteoporosis. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules encoding fusion polypeptides capable of binding a cytokine to form a non-functional complex, useful for treating cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis.
IL-6 trap; cytokine; antagonist; CNTF; re
cytostatic; immunomodulator; osteopathic.
                                                                                                                                                                                                                                                                        AAY92204 standard; protein; 1168 AA
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22-MAR-2001; 2001US-00787835.
                                                                                       Fusion polypeptide 412, IL-6 trap
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DB; AAD63741.
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YANCOPOULOS G
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                                                                                                                                                                                                                                                                                                                                                                                                                          GEWSEWSPEAMGTPWTESRSPPAENEVSTPMELL 334
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Pred. No. 7.8e
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                                  receptor;
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                               fusion protein;
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VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS

120 120 60

CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180 VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS

PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV

> 240 180

<u>.</u>

Gaps

181 121 121 61 61

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This sequence shows fusion polypeptide 412, which is capable of binding cytokine II-6 to form a non-functional complex. The invention concerns croduction of antagonists to any cytokine that utilizes an alpha compendicity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-cross functional intermediate which then binds to a second beta signal component causing beta-receptor dimerization, the soluble calpha specificity determining component of the receptor (sR-alpha) and the extracellular domain of the first beta signal transducing component of the extracellular domain of the first beta signal transducing component continues to the cytokine such as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are cytokine to form a non-functional complex. The receptor components are cytokines. The invention provides the basis for the development of II-c fanctional intermediate complex, consisting of the ligand, its alpha creceptor and its beta-1 receptor component, can be formed, it will conclinate the action of the ligand. Effective antagonists of II-c extracellular domain of gpl30. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessbile to form a signal cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia
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Matches 330
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19-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule for treating cytokine-related diseases disorders encodes a fusion polypeptide capable of binding a cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGE-) REGENERON PHARM INC
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99US-00313942
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Score 1783; DB 3;
Pred. No. 1.7e-110;
1; Mismatches 0;
                                   Length 1168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding fusion polypeptides capable of binding a cytokine to form a non-functional complex, useful for treating cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis
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(YANC/)
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22-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytokine
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                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors for treating cytokine-related diseases or disorders e.g. cancer, cachexia, arthritis and osteoporosis. The present sequence is human cytokine trap protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                  Sequence 1168
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achexia; arthritis; cytostatic; osteopathic; therapy; human.
                                                                                                  MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                      Yancopoulos
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Pred. No. 1.7e-110;
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The invention relates to selecting or designing a compound that interacts with the interleukin-6 receptor (IL-6R) via assessing and obtaining the stereochemical complementarity between the compound and a topographic region of the receptor and testing the compound for its ability to modulate an activity associated with the receptor. Also disclosed is the crystal structure of the IL-6R alpha chain. The compounds of the
                                                                                                                                                                                                               WPI; 2003-558820/52.
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Smith BJ;
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                                                                                                                                                                or designing compound interacting r treatment of e.g. AIDS, involves
                                                                                                                                               modulate activity of
                                                                                                                                                                                                                                                               Simpson RJ,
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/14bel= Tryptophan-arginine
/note= "Forms a left-handed
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/label= Tryptophan-arginine_ladder
/note= "Forms a left-handed 310 helix structure"
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Matches 325; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             Hybrid peptide; malaria parasite; Plasmodium falciparum; red blood cell; cytokine receptor; glycophorin binding pe GBP 130; GBPH; glycophorin binding peptide homologue; gly
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Pred. No. 7.6e-110;
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09-MAR-1995

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23-AUG-1994;
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llarity 69.6%;
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capable of binding a red blood
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Pred. No. 6e-109;
5; Mismatches 73;
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c; osteopathic; antipsoriatic; interleukin-6 receptor; II-
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to form a homodimer"
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to form a homodimer"
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The invention relates to selecting or designing a compound that interacts with the interleukin-6 receptor (IL-6R) via assessing and obtaining the stereochemical complementarity between the compound and a topographic region of the receptor and testing the compound for its ability to modulate an activity associated with the receptor. Also disclosed is the crystal structure of the IL-6R alpha chain. The compounds of the invention act as cytokine receptor modulators and may be useful in the prevention and treatment of diseases associated with signalling by IL-6R such as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis, prostate cancer, Castleman's disease, AIDS, mesangial proliferative glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.
                                                                                                                                                                  Selecting or designing compound interacting with interleukin receptor, useful for treatment of e.g. AIDS, involves assessing and testing compound to modulate activity of receptor.
                                                                                                                                                                                                                                           Varghese JN,
Smith BJ;
                                                                                                                                                                                                                                                                                          (CSIR )
(LUDW-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CC with the interleukin-6 receptor (II-6R) via assessing and obtaining the CC stereochemical complementarity between the compound and a topographic cregion of the receptor and testing the compound for its ability to CC modulate an activity associated with the receptor. Also disclosed is the CC crystal structure of the II-6R alpha chain. The compounds of the CC invention and treatment of diseases associated with signalling by II-6R prostate cancer, Castleman's diseases, AIDS, mesangial proliferative CC prostate cancer, Castleman's disease, AIDS, mesangial proliferative CC prostate cancer, Castleman's disease, AIDS, mesangial proliferative CC prostate cancer, Castleman's disease, AIDS, mesangial proliferative to the naturally occurring II-6 receptor ligand as well as a rational basis CC for the development of ligands for specific therapeutic applications. The information provided by the II-6R crystal structure will facilitate a CC substitution. Note: The current sequence is not shown within the CC substitution but was created by the invention which contains a C192A CC substitution but was created by the invention which contains a C192A contains a C192A contains and contains a C192A contains a created by the invention which contains a C192A contains a created by the indexer using the human II-6R alpha
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Best Local Similarity
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Smith BJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                               chain wild-type protein sequence
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   SPPAENEVSTPMQALTTNKDDDNIL
                                               ERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEBFGQGEWSEWSPEAMGTPWTESR
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Matches 323; Conserv
                                                                                                                                                                                                                                                                                         Sequence 325
                                                                                                                                                                                                                                                                                                               The invention relates to the production of human interleukin-6 receptor (IL-6R) protein in the fungus Pichia pastoris. The fungus was transformed with an expression vector (pOIC9-A20LL) containing a gene encoding an IL-6R protein having an immunoglobulin-like region and cytokine receptor region and spanning amino acids from Leu20-Ala323. The human IL-6R region was PCR amplified using the primers AAA70702-A70703. This sequence represents the recombinant IL-6R protein of the invention
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                                                                                                                                              RLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRST
ERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESR
                                                                                                                                RLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRST
                       SKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRA
                                       SKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRA
                                                                           PSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVG
                                                                                           PSĽTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVG
                                                                                                                                                                                   LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAEMGR
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99.4%;
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                                                                                                                                                                                                                                    Score 1748; DB 3;
Pred. No. 7.7e-109;
0; Mismatches 2;
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                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                              The invention relates to a method for the preparation of bovine interleukin 12 (BoILI2). BoILI2 consists of a heterodimer of p35 and p40 subunits. BoILI2 is produced by introducing into a host cell, recombinant vectors containing genes encoding the p35 and p40 subunits. This sequence represents the bovine ILI2 p35 subunit. Interleukin 12 is used for the
                                                                                                                                                                                                                                                                   Sequence 325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of bovine interleukin 12 comprising using a vector containing the gene encoding it, useful for the prevention and treatment of chronic and opportunistic infections.
                                                                                                                                                                                                                                                                                         prevention infections
                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 8; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP2000157274-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiinfective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine interleukin-12 p35 subunit protein.
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                                                                                                                                       80 RLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRST
                                                                                                                                                                                       20 LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGR
                                                                                                                                                                                                                       323;
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ERSKTETTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPBAMGTFWTESR
                                   SKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRA
                                                 SKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRA
                                                                                                                            LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAEMGR
                                                                                PSITTKAVILLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVG
                                                                                                    PSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVG
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                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                     treatment of chronic infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bovine;
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                                                                                                                                                                                                                                 Score 1748; DB 3;
Pred. No. 7.7e-109;
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RESULT 40
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KW ostee
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XX Homo
OS Synch
XX Key
FT Domai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; prostate cancer; Castleman's disease; AIDS; human; mesangial proliferative glomerulonephritis; Kaposi's sarcoma; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nephrotropic; osteopathic; antipsoriatic; interleukin-6 receptor;
alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; 
                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human interleukin 6 receptor alpha chain mutant peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO23015 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; antirheumatic;
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to form a homodimer"
6. .174
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                                           to form a
190. .193
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132. .141
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                                                                            166. .172
/note= "Dimer interface,
--- form a homodimer"
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133. .138
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                                                                                                                                                      160. .168
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            'note=
                                 note=
                                                                note= "Dimer interface,
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                                                                                                                                            note=
                                                                                                                                                                   'note= "L2 loop"
                                                                                                                                                                                                                                                                                                                        form a homodimer"
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                       .299
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                                                                                                                                                                                                                                                                             "Double proline
                                                                                                                                                                                                                                                                                                    "D2
                                                                                                                                                                                                                                                                                                                                                                   "Dimer interface,
                                  "L4 loop"
                                                                                                                                            "L3 loop"
                                                                                                                       "SSFY motif"
                                                                                                                                                                                                                                                                                                    domain"
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                                                                                                                                                                                                    which IL-6R monomers interact
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   The invention relates to selecting or designing a compound that interacts with the interleukin-6 receptor (IL-6R) via assessing and obtaining the stereochemical complementarity between the compound and a topographic region of the receptor and testing the compound for its ability to modulate an activity associated with the receptor. Also disclosed is the crystal structure of the IL-6R alpha chain. The compounds of the invention act as cytokine receptor modulators and may be useful in the prevention and treatment of diseases associated with signalling by IL-6R such as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis, prostate cancer, Castleman's disease, AIDS, mesangial proliferative glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
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                                                                                                                                                        Selecting or designing compound interacting with interleukin receptor, useful for treatment of e.g. AIDS, involves assessing and testing compound to modulate activity of receptor.
                                                                                                                                                                                                                                                                                                                          16-SEP-2002; 2002WO-AU001255
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                                                                                                                                    Example 1;
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LUDWIG INST CANCER RES.
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                                                                                                                                   Page; 361pp; English
                                                                                                                                                                                                                                                            INST MEDICAL
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214
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/note= "Forms a left-handed 310 helix structure"
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/note= "Forms
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Best Local Similarity 99.7%;
Matches 324; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The method provides enhanced stereochemical complementarity relative to the naturally occurring IL-6 receptor ligand as well as a rational basis for the development of ligands for specific therapeutic applications. The information provided by the IL-6R crystal structure will facilitate a more accurate understanding of how the binding of a ligand leads to signal transduction. The current sequence is that of the human IL-6R alpha chain mutant protein of the invention which contains a W214N substitution. Note: The present sequence is not shown within the specification but was created by the indexer using the human IL-6R alpha chain wild-type protein sequence (AAO23014)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 325 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGR
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1 MLAVGCALLAALLAAPGAAL.....LILRSFKEFLQSSLRALRQM 543
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1: pir1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	U)	4.	ω	N	۳	Regult No.
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protactin receptor		rec	interleukin-6 sign	membrane glycoprot	Œ	prolactin receptor		prolactin receptor	interleukin 12B pr	Soluble interleuki	ς.	כסי	ciliary neurotroph	interleukin-11 rec	interleukin-11 rec	interleukin-6 prec	interleukin-6 prec		interleukin-6 prec	9	interleukin 6 - pi	prointerleukin 6 -	interleukin-6 prec	interleukin-6 rece	interleukin-6 prec	interleukin-6 rece	interleukin-6 rece		Description

## ALIGNMENTS

A;Gene: GDB:ILGR A;Cross-references: GDB:127966; OMIM:147880 A;Map position: 1q21-1q21 C;Superfamily: ciliary neurotrophic factor receptor; C;Ckeywords: acute phase; cytokine receptor; glycoprote F;1-19/Domain: signal sequence #status predicted <sig-10-163 #status="" <crs-19:364-386="" <ext-10-163="" <imm2-19:11-309="" <tmm<="" cytokine="" domain:="" extracellular="" homology="" immunoglobulin="" predicted="" receptor="" th="" transmembrane=""><th>A;Residues: 1-468 <sch> A;Cross-references: EMBL:x58298; NID:g32580; PIDN:CAA41; A;Experimental source: hepatoma cell line Hep62 R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M J. Exp. Med. 170, 1409-1414, 1989 A;Title: Soluble cytokine receptors are present in norma A;Reference number: A61459; MUID:90010793; PMID:2529343 A;Accession: A61459 A;Molecule type: protein A;Residues: 20-49 <nov> C;Comment: Through this receptor, interleukin-6 induces C;Comment: This growth factor receptor does not have a connections.</nov></sch></th><th>A; Residues: 1-468 &lt; YAM&gt; A; Residues: 1-468 &lt; YAM&gt; A; Cross-references: UNIPROT: P08887; GB:M20566; NID:g338 R; Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawan Proc. Jpn. Acad. 64, 209-211, 1988 A; Title: Molecular structure of interleukin 6 receptor. A; Reference number: JU0080 A; Rocession: JU0080 A; Molecule type: mRNA A; Residues: 1-468 &lt; YA2&gt; R; Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hi Biochem. J. 277, 659-664, 1991 A; Fitle: Structural and functional studies on the human A; Reference number: S17468; MUID:91336983; PMID:1872801 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA</th><th>RESULT 1 A41242 interleukin-6 receptor precursor - human interleukin-6 receptor precursor - human N;Contains: interleukin-6 receptor, soluble form C;Species: Homo sapiens (man) C;Date: 27-Mar-1992 #sequence revision 02-Dec-1994 #tex C;Accession: A41242; JU0080; S17468; A61459; S14621 R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawan Science 241, 825-828, 1998 A;Title: Cloning and expression of the human interleuki A;Reference number: A41242; MUID:88305347; PMID:3136546 A;Accession: A41242 a.MOlecula type: MENA</th></sig-10-163>	A;Residues: 1-468 <sch> A;Cross-references: EMBL:x58298; NID:g32580; PIDN:CAA41; A;Experimental source: hepatoma cell line Hep62 R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M J. Exp. Med. 170, 1409-1414, 1989 A;Title: Soluble cytokine receptors are present in norma A;Reference number: A61459; MUID:90010793; PMID:2529343 A;Accession: A61459 A;Molecule type: protein A;Residues: 20-49 <nov> C;Comment: Through this receptor, interleukin-6 induces C;Comment: This growth factor receptor does not have a connections.</nov></sch>	A; Residues: 1-468 < YAM> A; Residues: 1-468 < YAM> A; Cross-references: UNIPROT: P08887; GB:M20566; NID:g338 R; Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawan Proc. Jpn. Acad. 64, 209-211, 1988 A; Title: Molecular structure of interleukin 6 receptor. A; Reference number: JU0080 A; Rocession: JU0080 A; Molecule type: mRNA A; Residues: 1-468 < YA2> R; Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hi Biochem. J. 277, 659-664, 1991 A; Fitle: Structural and functional studies on the human A; Reference number: S17468; MUID:91336983; PMID:1872801 A; Molecule type: mRNA	RESULT 1 A41242 interleukin-6 receptor precursor - human interleukin-6 receptor precursor - human N;Contains: interleukin-6 receptor, soluble form C;Species: Homo sapiens (man) C;Date: 27-Mar-1992 #sequence revision 02-Dec-1994 #tex C;Accession: A41242; JU0080; S17468; A61459; S14621 R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawan Science 241, 825-828, 1998 A;Title: Cloning and expression of the human interleuki A;Reference number: A41242; MUID:88305347; PMID:3136546 A;Accession: A41242 a.MOlecula type: MENA
A;Gene: GDB:IL6R A;Gene: GDB:IL6R A;Gene: GDB:IL6R A;Gene: GDB:IL6R A;Gene: GDB:IL6R A;Map position: 1q21-1q21 C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunogl C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunogl C;Superfamily: ciliary neurotrophic factor receptor; transmembrane protein F;1-19/Domain: signal sequence #status predicted <sig>F;20-468/Product: interleukin-6 receptor #status predicted <mat> F;20-468/Product: interleukin-6 receptor #status predicted <mat> F;20-363/Domain: cytokine receptor homology <inm2> F;30-383/Domain: cytokine receptor homology <cr8> F;121-309/Domain: transmembrane #status predicted <tmm></tmm></cr8></inm2></mat></mat></sig>	A;Residues: 1-468 <sch> A;Cross-references: EMBL:X58298; NID:g32580; PIDN:CAA41231.1; PID:g32581 A;Cross-references: EMBL:X58298; NID:g32580; PIDN:CAA41231.1; PID:g32581 A;Experimental source: hepatoma cell line HepG2 R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M. J. Exp. Med. 170, 1409-1414, 1989 A;Title: Soluble cytokine receptors are present in normal human urine. A;Reference number: A61459; MUID:90010793; PMID:2529343 A;Accession: A61459 A;Accession: A61459 A;Accession: A61459 A;Accession: Torough this receptor, interleukin-6 induces proliferation, activation, and di C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, and di C;Comment: This growth factor receptor does not have a tyrosine kinase domain.</sch>	A; Residues: 1.468 < YAM> A; Residues: 1.468 < YAM> A; Cross-references: UNIPROT: P08887; GB:M20566; NID:g33845; PIDN: CAA31312.1; PID:g33846 A; Cross-references: UNIPROT: P08887; GB:M20566; NID:g33845; PIDN: CAA31312.1; PID:g33846 A; Cross-references: UNIPROT: P08887; GB:M20566; NID:g33845; PIDN: CAA31312.1; PID:g33846 A; Yamasaki, K.; Tags. T.; Hitata, Y.; Xawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; A; Reference number: JU0080 A; Reference number: JU0080 A; Residues: 1-468 < YA2> A; Residues: 1-468 < YA2> A; Residues: 1-468 < YA2> A; Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, Biochem. J. 277, 659-664, 1991 A; Title: Structural and functional studies on the human hepatic interleukin-6 receptor. N A; Reference number: S17468; MUID:91336983; PMID:1872801 A; Noteculae type: mRNA A; MACESSBION: S17468	RESULT 1 A41242 A1274

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                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P22272; GB:X51976; NID:g53548; PIDN:CAA36238.1; PID:g53549 C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immun C;Keywords: cytokine receptor; transmembrane protein C;Keywords: cytokine receptor; transmembrane protein.
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A; Residues: 1-440 <SUG>
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A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen A;Reference number: JL0144; MUID:90278354; PMID:2112585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-6 receptor precursor (clone lambda P1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec_1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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F;47-96/Disulfide bonds: #status predicted
F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
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CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA
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                                                                                                                                                                                                                                             Conservative
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96.5%;
                                                                                                                                                                                                                                   33.4%; Score 954.5; DB 2; 50.1%; Pred. No. 1.5e-58; tive 52; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Pred. No. 2.8e-125;
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                                                                                                                                                                                                                                                                                 Length 440;
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A,Molecule type: mRNA
A;Residues: 1-373,'R',375-460 <FIO>
A;Cross-references: EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunogl
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-460/Product: interleukin-6 receptor #status predicted <MAT>
F;410-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;117-306/Domain: cytokine receptor homology <CRS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0145
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-6 receptor precursor (clone lambda 301) - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0145; S14543
C;Accession: JL0145; S14543
J. Expita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, J. Exp. Med. 171, 2001-2009, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 VPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                  h 33.4%; Score 954.5; DB 2; Similarity 50.1%; Pred. No. 1.6e-58; 88; Conservative 52; Mismatches 122;
         ILEGDKVYHI VSLCVANS VGSKSSHNEAFHSLKMVQPDPPANLVVSAIPGRPRWLKVSWQ
                                                VPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQ
                                                                                                                                            CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA 179
                                                                                                                                                                                                                       VLRKPAAGSHBSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEEPQLS 120
                                                                                                                                                                                            VY----SGSQNREWTTTGNTLVLRDVQLSDTGDYLCSLNDHLVGTVPLLVDVPPEEPKLS
                                                                                                                                                                                                                                                                                                                   MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                CFRKNPLVNAICEWRPSSTPSPTTKAVLFAKKINTTNGKSDFQVPCQYSQQLKSFSCQVE 176
                                                                                                                                                                                                                                                                                           MLTVGCTLLVALLAAPAVALVLGSCRALEVANGTVTSLPGATVTLICPGKEAAGNVTIHW
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PID: 949726

gene

Gaps

60

236 239

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A;Molecule 1-212 <TON>
A;Residues: 1-212 <TON>
A;Residues: 1-212 <TON>
A;Cross-references: GB:M29150; NID:g186349; PIDN:AAA5915-
A;Cross-references: GB:M29150; NID:g186349; PIDN:AAA5915-
R;Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.;
R;Haegeman, G.; Content, J.; Volckaert, G.; Derynch, R.;
R;Haegeman, G.; Content, R.; Ling, R.; 
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                                                                                               A; Molecule type: mRNA
A; Residues: 1-212 < MAY >
                                                                                                                                                                                         A; Reference number: A25921;
A; Accession: A25921
                                                                                                                                                                                                                                 R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.
Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
A;Title: Anti-beta-interferon antibodies inhibit the increased expression
A;Reference number: A25921; MUID:87067433; PMID:3538015
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:X04403
A;Experimental source: fibroblast
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A; Residues: 1-212 < HAE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-212 <HIR>
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A; Residues: 1-212 <ZIL>
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C;Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B27
R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimot
EMBO J. 6, 2939-2945, 1987
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Cross-references: GB:M14584;
Wong, G.G.; Witek-Giannotti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Cross-references: GB:X04430; NID:g32673; PIDN:CAA28026.1; PID:g32674;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda,
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2529-2537, 1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGQWSEWSPEVTGTPWIAEPRTTPA-GILWNPTQVSVEDSANHEDQYESSTEATSV----
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     J.;
     :g184628; PIDN:AAA52728.1; PID:g306910
Hewick, R.M.; Clark, S.C.; Ogawa, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:AAA59154.1; PID:g307063
Derynck, R.; Tavernier, J.;
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A;Experimental source: FS-4 fibr
A;Note: sequence extracted from
A;Note: this 23-25K form contain
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A;ACCEBBLUI. ..... Protein
A;Molecule type: protein
A;Residues: 30-43 <YAM'>
A;Residues: 30-43 <YAM'>
A;Residues: 30-43 <YAM'>
A;Rirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
A;Title: Human beta-cell differentiation factor defined by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 29-42 <HIR2>
R,Roda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi,
R,Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi,
Anticancer Res. 11, 961-968, 1991
A,Title: Purification and characterization of human fibrob
A,Reference number: A61159; MUID:91290785; PMID:1648338
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R;Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
J. Immunol. 144, 1808-1816, 1990
A;Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved A;Reference number: A60400; MUID:90171574; PMID:2307841
                                                                                                                                                                                                                                                                                                                                                                   R;May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, Cytokine 3, 204-211, 1991
A;Title: Marked cell-type-specific differences in A;Reference number: A48419; MUID:91355644; PMID:18
A;Accession: A48419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: fibroblast R;Ming, J.B.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A. R;Ming, J.B.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A. J. Mol. Cell. Immunol. 4, 203-212, 1989 A;Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor for A;Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor for A;Reference number: A61462; MUID:90121567; PMID:2610854
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A; Residues: 28-51,'X',53-57,'X',59,'X',61 < VAN1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GB:M54894; NID:g186351; PIDN:AAC41704.1; PID:g186352 R;Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, IJ. Immunol. 139, 4116-4121, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behring Inst. Mitt. 83, 40-47, 1988
A; Title: Interleukin 6: Identification as a hematopoietic A; Reference number: I52193; MUID:89193317; PMID:3266463
                                                                                                                                                                                                   A;Residues: 30-37,'X', 39-40 «MAY2»
A;Experimental source: FS-4 fibroblasts
A;Note: sequence extracted from NCBI backbone
A;Note: this 28-30K form contained both N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 30-42 < NOD>
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                                                                                                                                A; Molecule type: protein
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                                                                                                        28-40 <MAY3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al source: leukocyte-conditioned medium
Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -212 <WON>
3-4 fibroblasts
ad from NCBI backbone (NCBIP:63787)
contained O-linked but not N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of human fibroblast PMID:1648338
                                                                                                                                                                                                                                                                                                                                                                                                         nces in glycosylation PMID:1883960
                                                                                                                                                                                                          and
                                                                                                                                                                                                          O-linked carbohydrate; a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colony-stimulating factor.
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De Ley, M.;
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carbohydrate

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interleukin-6 receptor precursor - rat

N;Alternate names: IL-6 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C;Accession: A37986

R;Baumann, M.; Baumann, H.; Fey, G.H.

J. Biol. Chem. 265, 19853-19862, 1990

A;Title: Molecular cloning, characterization and functional expression of the rat liver

A;Reference number: A37986; MUID:91060602; PMID:2174054

A;Recession: A37986

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P22273; GB:M58587; GB:J05668; NID:g204921; PIDN:AAA41431.1;
C;Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is es
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: acute phase; cytokine receptor; transmembrane protein

F;1-19/Domain: signal sequence #status predicted <SIG>
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A;Contents: annotation; modified sites in recombinant protein from CHO cells
R;Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
Arch, Biochem. Biophys. 272, 144-151, 1989
A;Title: Disulfide structures of human interleukin-6 are similar to those of human granu
A;Reference number: S04981; MUID:9286115; PMID:2472117
A;Contents: annotation; disulfide bonds in recombinant protein
A;Reck, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
Biochemistry 33, 5146-5154, 1994
A;Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
A;Reference number: A54253; MUID:94227044; PMID:8172889
A;Contents: annotation; lability and functional significance of each disulfide bond
C;Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factor lobulin secretion). It therefore appears to function as an autoregulator of cell growth
C;Comment: This protein plays a regulatory role in various host defense mechanisms and e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
A37986
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A;Introns: 7/1, 70/3; 108/3; 157/3

C;Superfamily: interleukin-6

C;Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; ;

F;1-27/Domain: signal sequence #status predicted <SIGs

F;28-212/Product: interleukin-6, long form #status experimental <MATLs

F;30-212/Product: interleukin-6, short form #status experimental <MATSs

F;30-212/Product: interleukin-6, short form #status experimental

F;30-111/Disulfide bonds: #status experimental

F;73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

F;166/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

F;172/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A;Gene: GDB:IL6
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A; Molecule type: mRNA
A; Residues: 1-208 <SWI>
A; Cross-references: UNIPI
C; Genetics:
A; Gene: II-6
C; Superfamily: interleuk:
C; Keywords: cytokine; gro
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A;Accession: T09216
A;Status: preliminary; tra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-6 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 11-Jun-1999 #sequence_revision 11-
C;Accession: T09216
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F;20-362/Domain: extracellular #status predicted <EXT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;363-385/Domain: transmembrane #status predicted <TMM>
F;363-885/Domain: intracellular #status predicted <INT>
F;366-462/Domain: intracellular #status predicted <INT>
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                  cytokine; growth
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                                                          SSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQ
                                                                                                                                       ATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAQEEFGQGEWSEWSPEAMGTPW-TESRSPPAENEVSTPMQALTTNKDDDNILFRDSANA
ARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFK
                                 NSKEVLAENNLNLPKMAEKDGCFQSGFNQETCLMKITTGLSEFQIYLEYLQNEFKGEKEN
                                                                                                       ATAFPT---PLPLGEDETTSNGP---LLTTADKTKQHIKYILGKISALKNEMCNNFSKCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA 179
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                                                                                                                                                                                                                                                                     interleukin-6
                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                       UNIPROT:Q95181; EMBL:U64794; NID:g2654387; PID:g2654388
                                                                                                                                                                            20.0%; Score 571.5;
58.5%; Pred. No. 1.96
ative 32; Mismatches
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48.4%;
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Pred. No. 1.7e-51;
0; Mismatches 119;
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R;Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A;Title: Expression of interleukin-6 in porcine, ovine, A;Reference number: I46590; MUID:92360284; PMID:1497880
A;Accession: I46590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Crose-reference
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C;Species: Sus s
C;Date: 21-Feb-1
                                                                                                   A;Gene: בביט
C;Superfamily: interleukin-6
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R;Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
Cytokine 3, 269-276, 1991
A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and A;Reference number: 146621; MUID:91338547; PMID:1873476
A;Accession: 146621
                                                                                                                                                                                                                                                                                                                C; Date: 21-Feb-1997
C; Accession: I46590
                                                                                                                                                                                                                                                                                                                       C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
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C;Genetics:
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A; Residues: 1-212 < RIC>
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;Species: Sus scrofa domestica (domestic pig)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
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Best Local Similarity
Matches 112; Conserv
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                                                                  Query Match
Best Local
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                                                                    Similarity
ATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCE 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATSLPVBFMPVPPG----EDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFKEFLQSSLRALRQM 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.6%; Score 559.5; DB 2 ilarity 57.1%; Pred. No. 1.3e-31; Conservative 32; Mismatches 43
                                                   Conservative
                                                               19.5%;
                                                 32;
                                                                 Score 557.5; DB 2; Pred. No. 1.8e-31;
                                                   Mismatches
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interleukin-6 precursor - bovine
(;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A56610; S22162
R;Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
DNA Seq. 2, 411-413, 1992
A;Title: Nucleotide sequence of bovine interleukin-6 cDNA.
A;Reference number: A56610; MUID:93076003; PMID:1446077
A;Accession: A56610
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K. Proc. Soc. Exp. Biol. Med. 204, 301-305, 1939
A;Title: Molecular cloning and characterization of a cDNA encoding A;Reference number: I46084; MUID:94052249; PMID:8234373
A;Accession: I46084
A;Residues: 1-208 <DRO>
A;Residues: 1-208 <DRO>
A;Cross-references: UNIPROT:P26892; EMBL:X57317; NID:g2193; PIDN:CAA40572.1;
A;Experimental source: BLV induced B cell-lymphosarcoma
A;Note: sequence extracted from NCBI backbone (NCBIP:118917)
C;Superfamily: interleukin-6
C;Keywords: cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin 6 - cat
C;Species: Felis silvestris catus (domestic cat)
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A; Residues: 1-207 <BRA>
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C;Accession: I46084
                                                                                                                                                                   A; Molecule type: mRNA
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Best Local
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C;Species: Ovis orientalis aries, Ovis ammon aries C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S29549
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                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34247
R;Northemann, W; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
R;Northemann, W: Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
A;Title: Structure of the rat interleukin 6 gene and its expression in macr.
A;Reference number: A34247; MUID:89380206; PMID:2789217
A;Accession: A34247
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A;Residues: 1-208 <EBR>
A;Cross_references: UNIPROT:P29455; EMBL:X68723
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A;Status: preliminary
A;Molecule type: mRNA
,A;Residues: 1-211 <NOI
                                                                                                                                                                                 N;Alternate names: IL-6
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ilarity 51.6%;
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A;Cross-references: UNIPROT:P20607; GB:M26744; NID:g204915; PIDN:AAA77659.1; PID:g204916 C;Superfamily: interleukin-6 C;Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text change 09-Jul-2004
C;Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486;
R;Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
R;Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
A;Title: Genomic structure of the murine IL-6 gene. High degree conservation A;Reference number: A30531; MUID:89035525; PMID:3263439
A;Accession: A30531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P08505; GB:M20572; NID:g198369; PIDN:AAA39302.1; PID:g387386 R;Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Simg Bur. J. Immunol. 18, 193-197, 1988 Bur. J. Immunol. 18, 193-197, 1988 Bur. J. CONA cloning of murine interleukin-HPI: homology with human interleukin 6. A;Reference number: A27610; MUID:88166883; PMID:2965020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702 R;Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Cop J. Immunol. 142, 1372-1376, 1989 A;Title: The murine II-6 gene maps to the proximal region of chromosome A;Reference number: A30571; MUID:89124383; PMID:2563387 A;Accession: A30571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin-6 precursor - mouse N_{\ell}Alternate\ names:\ B-cell\ hybridoma\ growth\ factor;\ B-cell\ stimulating
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                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
R;Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
Ext. J. Biochem. 176, 187-197, 1988
A;Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and A;Reference number: S01323; MUID:88329059; PMID:3262059
                                                                                     Nucleic Acids Res. 18, 6455, 1990
A;Title: Cloning and sequence analysis of t
A;Reference number: S12103; MUID:91057159;
A;Accession: S12103
                                                                                                                                                                           A;Molecule type: protein
A;Residues: 25-166,'X',188-211 <SIM>
A;Residues: 25-166,'X',188-211 is inconsistent with that
A;Note: the sequence from Fig. 11 is inconsistent with that
R;Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-211 < VAN>
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A;Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
                              A;Molecule type: mRNA
A;Residues: 1-211 <GRE>
                                                                                                                                                                                                                                                                                                                       A; Accession: S01323
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A; Residues: 5-211 < MOC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 ATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCE 410
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Similarity 39.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSF 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSDDALSENNIKLPEIQRNDGCFQTGYNQEICLLKICSGLLEFRFYLEFVKNNLQDNKKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEFLKVTMRSTRO
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Pred. No. 2.5e-20;
53; Mismatches 59;
                                                                                                                          the cDNA for murine; PMID:2243807
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A;Map position: 5
A;Introns: 7/1; 68/3; 106/3; 156/3
C;Superfamily: interleukin-6
C;Keywords: Castleman's disease; cytokine; growth factor; immunoregulation;
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-211/Product: interleukin-6 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 77-98 <SHA>
R;Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A;Title: DNA rearrangement and constitutive expression <a href="#">A;Reference number: S10241; MUID:90171860; PMID:2106569">A;A;Cccession: S10241</a>
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A;Title: The myeloid blood cell differentiation-inducing protein MGI-2A is in A;Reference number: A60799; MUID:89062753; PMID:3264198
A;Accession: A60799
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A; Residues: 25-39; X', 41-42, 'X', 44-45 < VSN>
A; Residues: 25-39; X', 41-42, 'X', 44-45 < VSN>
R; Chiu, C. P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
R; Chiu, C. P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A; Title: Multiple biological activities are expressed by a mouse
A; Reference number: A40486; MUID:89017145; PMID:3262872
A; Accession: A40486
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A;Molecule type: protein
A;Residues: 38-60;75,'X',77-79;176-203
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A; Residues: 1-6 <BLA>
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A; Title: Purification and NH2-terminal amino acid sequence of a
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Best Local S
Matches 76
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                                                                                                                          471
                         531
                                                                                                                                                                                                                                                                           23
                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                n 13.1%; Score 374.5; DB 1; Similarity 39.6%; Pred. No. 8.5e-19;
                                                                                                                                                                        NDDALAENNLKLPBIQRNDGCYQTGYNQBICLLKISSGLLBYHSYLBYMKNNLKDNKKDK
                                                                                                                                                                                                                          SKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRF-ESSEEQ
                                                                                                                                                                                                                                                                                                                       TSLPVEFMPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCES
                         EFLOSSLRALRO 542
                                                                           ARVLQRDTETLIHIFNQEVKDLHKİVLPTPISNALLTDKLESQKEWLRTKTIQFILKSLE
                                                                                                                       ARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFK
                                                                                                                                                                                                                                                                           TAFPTS---QVRRGDFTED-TTPNR-PVYTTSQVGGLITHVLWEIVEMRKELCNGNSDCMN
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interleukin-11 receptor alpha chain - human C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence revision 29-Mc;Accession: I37891; G01970; G01971
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A;Gene: Bt12/IL11
C;Superfamily: ciliary neurotrophic factor receptor;
C;Keywords: cytokine receptor
E;120-310/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432 <HIL>
A;Cross-references: EMBL:U14412; NID:g576454; PIDN:AAA53248.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossier Dev. Biol. 166, 521-542, 1994
A;Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embryoger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48343; S51619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for high A;Reference number: S51619; MUID:95045367; PMID:7957045 A;Accession: S51619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q64385; EMBL:X74953; NID:g673437; PIDN:CAA52908.1; PID:g6734: R;Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.; EMBO J. 13, 4765-4775, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: I48343
A; Accession: I48343
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Best Local
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                                                                                                                                                MVXDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESRSPPAENEVS
                                                                                                                                                                                                                    LOSILREDEPOGLEVESVEGYERRLHASWTYPASWERQPHFLLKFELQYRPAQHPAWST-
                                                                                                                                                                                                                                                                                                                                STGPWPC----PQDPLEASRCVVHGAEFWSEYRINVTEVNPLGA-----STCLLDVR
                                                                                                                                                                                                                                                                                                                                                                                   ----PCQYSQESQKFSCQLAVPEGDS--SFYIVSMCVASSVGSKFSKTQTFQGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHILVDVPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WVLRKPAAGSHPSRW-------AGMGRRLLLRSVQLHDSGNYSCYRA-GRPAGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSSSCSGLTRVLVAVATALVSSSSPCPQAWGPPGVQYGQPGRPVMLCCPGV--
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                                                   TPMQALTINKDDDNILFRDSANATSLPVEFMPVPPGEDSKDVAAPHRQPL 378
                                                                                                                                                                                                                                                                                                                                                                                                                                            VTLKLGFPPARPEVSC-QAVDYENFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQRESP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SAGT-PVSWFRDGDSRLLQGPDSGLGHRLVLAQVDSPDEGTYVCQTLDGVSGGM 104
                                                                                                                                                                                                                                                                       --GILQPDPPANITVTAVARNPRWLSVTWQDPHSW-NSSFYRLRFELRYRAERSKTFTTW
- PDWSQGHGQQLEAVVAQEDSPAPARP-SLQPDPRPLD-
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29-May-1998 #text\_change

09-Jul-2004

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ciliary neurotrophic factor receptor alpha chain - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 C;Accession: I58141; A47387 R;Ip, N.Y.; McClain, J.; Barrezueta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, Neuron 10, 89-102, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, i
Blood 86, 2534-2540, 1995
A;Title: Molecular cloning of two isoforms of a receptor i
A;Reference number: I37891; MUID:95399754; PMID:7670098
A;Accession: I37891
A;Cession: I37891
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <RES>
A;Cross-references: UNIPROT:Q16542; EMBL:Z38102; NID:g9956
R;Van Leuven, F.
Submitted to the EMBL Data Library, July 1995
Neuron 10, 89-102, 1993
A;Title: The alpha component of the CNTF receptor is required for
A;Reference number: IS8141; MUID:93152175; PMID:8381290
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A; Accession: G01970
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C;Genetics:
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A; Residues: 1-422 < VA
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-422 < VAN>
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ily: ciliary neurotrophic factor receptor; cytokine receptor homology; imm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTT-----KAVLLVRKFQNSPAEDFQE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WFRDGEPKLLQGPD-----SGLGHELVLAQADSTDEGTYICQTLDGALGGTVTLQLG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W-----VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRA-GRPAGTVHLLVD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAPPRPSLQPHPRLLDHRDSVEQVAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: Z38102; NID: g995653; PIDN: CAA86224.1; PID: g995
                                                                                                                                                                                                                                                                                                                                       354
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 185-260,'D',262-277 <CLA>
A;Residues: 185-260,'D',262-277 <CLA>
A;Residues: 185-260,'D',262-277 <CLA>
A;Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A;Experimental source: Sprague-Dawley, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:128471, NCBIP:128472)
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homo(;Keywords: growth factor receptor
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q08406; GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056 R;Clatterbuck, R.B.; Price, D.L.; Koliatsos, V.B. Proc. Natl. Acad. Sci. U.S.A. (222-226, 193 A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cent A;Reference number: A47387; MUID:93211934; PMID:8460125 A;Accession: A47387
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A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-372 <IPN
                   Development 121, 2681-2693, 1995
A;Title: Analysis of function and expression of the chick A;Reference number: S60614; MUID:95401882; PMID:7671828
A;Accession: S60614
                                                                                                                                                       growth promoting activity receptor alpha precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                              C; Accession: S60614
R; Heller, S.; Finn,
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A; Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSW-NSSFYRLRFELRYRAERSKTFTTWMVKDLQHHC-----VIHDAWSGLRHVVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAQEEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANAT
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                                                                                                                                                                                                                                                                                                                              STISSLAPPPITKICDPGE
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                                                                                                                 T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%;
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Pred. No. 5.3e-14;
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A;Cross-references: UNIPROT:P51641; EMBL:Z48 C;Superfamily: ciliary neurotrophic factor r C;Keywords: growth factor receptor F;2-89/Domain: immunoglobulin homology <IMM> F;114-294/Domain: cytokine receptor homology

receptor homology

<CRS:

A; Molecule type: mRNA A; Residues: 1-362 < HE

1-362 <HEL>

EMBL: Z48168; NID: g971417;

PIDN: CAA88184.1; PID: 93063;

immunog

receptor;

cytokine

receptor

1.4.2.

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A,Map position: 9p13-9p13

A,Map position: 9p13-9p13

C,Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog C,Superfamily: ciliary neurotrophic factor receptor; membrane protein; phosphatidylinositol F;1-20/Domain: signal sequence #status predicted <SIG»

F,21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>
F,219-91/Domain: immunoglobulin homology <IMM>
F,116-296/Domain: cytokine receptor homology <CRS>
F,146-89/Disulfide bonds: #status predicted
F,46-89/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: CNTF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40854; A56526
R;Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.E.; Squinto Science 253, 59-63, 1991
A;Title: The receptor for ciliary neurotrophic factor.
A;Reference number: A40854; MUID:91289158; PMID:1648265
A;Accession: A40854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-346,'S',348-372 <VAL>
A;Residues: 1-346,'S',348-372 <VAL>
A;Cross-references: GB:L38025; NID:g608654; PIDN:AAA91337.1; PID:g608656
C;Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylinosit
C;Comment: The CNTF receptor sequence appears to contain several PEST regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P26992; GB:M73238
R;Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, Genomics 25, 157-163, 1995
A;Title: Genomic organization and chromosomal localization of the human a A;Reference number: A56526; MUID:95293367; PMID:7774913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDLQHHC-----VIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESRSPP 322
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                                                            Conservative
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                                                                                    10.5%;
                                                       44;
                                                                                      Score 301; DB 1;
Pred. No. 2.2e-13;
                                                         red. No. 2.2e-13;
Mismatches 150
                                                            150;
                                                                                                           Length 372
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                         78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yanc
N;Alternate names: cytotoxic lymphocyte maturation factor 40% chain; natural killer c(;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A38957; B39359; S21688; B36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric A;Recession: A38957; MUID:91201875; PMID:1673147
A;Recession: A38957; MUID:91201875; PMID:1673147
A;Recession: A38957; MUID:91201875; PMID:1673147
A;Residues: 1-328 < WOL>
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interleukin 12B precursor [validated] -

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3

cyto

cell

A38957

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C;Genetics:
A;Gene: sIL-6R
C;Superfamily: c
C;Keywords: cyto
                                                                                                                                                                                                                                           A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-53 <RES>
                                                                                                                                                                                                                                                                                                                                                       R;Horiuchi, S.; Koyanagi, Y.; Zhou, Y.; Miyamoto, H.; Tanaka,
Bur. J. Immunol. 24, 1945-1948, 1994
A;Title: Soluble interleukin-6 receptors released from T cell
                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision
C;Accession: IS3394
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I53394
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                                                                                                                                                                                                                                                                                                  A;Reference number: I53394; MUID:94333499; A;Accession: I53394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble interleukin-6 receptor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                              ;Superfamily: ciliary neurotrophic factor receptor; ;Keywords: cytokine receptor
                                                                          Matches
                                                                                       Query Match
Best Local Similarity
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                     TPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVVQLRAQEEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRD 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSPLSNVVCEW----GPRSTPSLTTKAVLLVRKF---QNSPAEDFQEPCQYSQESQKFSCQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GTDLAPDLLNGSQLVLHGLEIGHSGLYACFHRDSWHLRHQVLLHVGLPPREPVLSCRS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:|| || || || : | | | || || : --AAAAVVYAQRHSPQE--APHVQYERLGSDVTLPC-GTANWD-AAVTWRVN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SANATSLPVEFMPVP----PGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVPEGDSSF-YIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIMVCEKDPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR--AGRPAGTVHLLVDVPPEEPQLSCFR 123
 TPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIIQVAAKDN-EIGTWSDWSVAAHATPWTEE----PRHLTTEAQAAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWOTPSTWPDPESFPLKFFLRYRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWODPHSW-NSSFYRLRFELRYRAERSKTFTTWMVKDLQHHC-----VIHDAWSGLR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRYMHLFSTIKYKVSISVSNALGHN-ATAITFDEFTIVKPDPPENVVARPVPSNPRRLEV
                                                                        Conservative
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                                                                                                                                                                                                                                                                                 translated from GB/EMBL/DDBJ
                                                                                       7.9%;
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                                                                        Score 226; DB; Pred. No. 2.6
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                                                                                                                                                                                                                                                                                                                      PMID:8056053
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                                                                                                             DB
                                                                                         6e-09
                                                                                                             <u>ب</u>
                                                                                                         Length
                                                                                                                                                                   cytokine
                                                                          Indels
 43
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                                                                                                                                                                                                                                                                                                                                                         or granulocyte/macrophage (
                                                                                                                                                                   receptor homology;
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A;Experimental source: lymphoblastoid cell line NC-37
C;Genetics:
A;Genetics:

                                                                                                                                 RESULT
JQ1655
        prolactin receptor precursor - chi
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revi
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A;Rosidues: 23-28,46-59,74-80,'X',94-130;161-169,'X',171-180;213-235;240-250;289-299,'X'
A;Residues: 33-28,46-59,74-80,'X',94-130;161-169,'X',171-180;213-235;240-250;289-299,'X'
A;Rexperimental source: lymphoblastoid cell line NC-37
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.; F
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lymphocyt
A;Reference number: A36055; MUID:90370873; PMID:2204066
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A;Reference number: S21688; MUID:92198015; PMID:1347984
A;Accession: S21688
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A;Title: Coexpression of two distinct genes is required to generate secreted b A;Reference number: A39359; MUID:91239523; PMID:1674604
A:Accession. Banaria
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Best Local S
Matches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 PQLSCFRKSPLSNVVCEW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 RWAGMGRRILLIRSVQLHDSGNYSCYRAGRPAGTVHLLV------DV------PPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
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                                                                                                                                                                                                                                                                                             -VFTDKTSATVICRKNASISVRAQDRYYSSSWSEWA
                                                                                                                                                                                                                                                                                                                                                                           CVIHDAWSGL-----RHVVQLRAQEEFGQGEWSEWS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLQLKPL-KNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NITVTAVARNPRWLSVTWQDPHSWNS--SFYRLRF--ELRYRAERSKTFTTWMVKDLQHH 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y----EYSVECQEDS---ACPANEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPE-EDGIT--WTL-----DQSS
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#sequence_revision 30-Sep-1993
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24.1%; Pred. No. 2.4e-06;
tive 51; Mismatches 135;
                                                                                          chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GPRSTPSLTTKAVLLVRKFQNSPAED
                                                                                                                                                                                                                                                                                             323
#text_change
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    09-Jul-2004
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c;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50455
R;Chen, X; Horseman, N.D.
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A;Cross-references: UNIPROT:Q04594; DDBJ:D13154; NID:g222848; PIDN:BAA02439
A;Cross-references: kidney
A;Experimental source: kidney
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-831/Product: prolactin receptor #status predicted <MAT>F;26-219/Domain: cytokine receptor homology <CRS1>F;36-219/Domain: cytokine receptor homology <CRS1>F;439-455/Domain: cytokine receptor homology <CRS1>F;439-462/Domain: transmembrane #status predicted <TMM>F;439-462/Domain: transmembrane #status predicted <TMM>F;439-455/Domain: cytokine receptor homology <CRS1>F;439-455/Domain: cytokine receptor homology <CRS1>F;439-456/Domain: transmembrane #status predicted <TMM>F;439-456/Domain: cytokine receptor homology <CRS1>F;439-456/Domain: 
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A;Title: Cloning, expression, and mutational analysis of the A;Reference number: I50455; MUID:94283267; PMID:7516866
A;Accession: I50455
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced
A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
A;Accession: JQ1655
A;Molecule type: mRNA
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 PAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDF 161
                                                                                                                                                                                                                                                                                                                                                     90
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                                                                                                                                                                                                                                                                                                                                                                                                                           <del>,</del> 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                              CVASSVGSKFSKTQTFQGCGILQPDPPANITV---TAVARNPRWLSVTWQDP--HSWNSS
                                                                                                                                                                                                      VLLVRKFQNSPAEDFQEPCQYSQESQK--FSCQLAVPEGDSSFYI------VSM
                                                                                                                                                                                                                                                                                DIGEWSEWSSER-----HIHIPNGESPPEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNY
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KATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNRKP-YLVLTWSPPPLADVRSG
                                                                                                                                                                                                                                                                                                                                              DSGNYSCYRAGRPAGTVHLLV---DVPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKA
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Pred. No. 0.00016;
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glycoprotein 130 - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.C.Species: Mus musculus (house mouse)
C.C.Species: Mus musculus (house mouse)
C.C.Species: Mus musculus (house mouse)
C.Accession: 149699; 148370
R.Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A.;Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer,
A.Reference number: 148370; MUID:92291532; PMID:1602143
A.Recession: 148699
A.;Status: translated from GB/EMBL/DDBJ
A.;Molecule type: mRNA
A.;Residues: 1-917 <RES>
A.;Cross-references: UNIPROT:Q00560; GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g1
A.;Accession: 148370
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Mol. Cell. Endocrinol. 89, 47-58, 1924
Molecular cloning of the bovine prolactin receptor
A;Reference number: 145971; MUID:93246019; PMID:1338725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I45971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I45971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R--WISVTWODPHSWN--SSFYRLRFELRYRAERSKTFTT-WMVKDLQHHCVIHDAWSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEKYLQIPTDFRIKDMVVWIIVGVLSSLICLVMSWTMVLKGYRMIAFILPPVPGPKIKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYLVOIRCKPD--HGYWSEWSPES 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFSCQLAVPEGDS-SFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKPYLWIKWSPPTMTDVKSGWFIIQYEIRLKPEKATDWETHFTLKQTQ--LKIFNLYPGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPEKPKLVKCRSPGKETFTCWWEPGADGGLPTNYTLTYHK----EGETLIHECPDYKTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 171; DB 2;
25.0%; Pred. No. 0.00041;
/ative 40; Mismatches 99
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A;Molecule type: mRNA
A;Rosidues: 1-917 <RE2>
A;Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817
C;Genetics:
A;Gene: gp130
C;Keywords: glycoprotein
C;Keywords: glycoprotein
F;134-314/Domain: cytokine receptor homology <CRS>
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A36337
A36337
membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
C;Accession: A36337
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A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology
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A;Title: Molecular cloning and expression of an IL-6 signal transducer, A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Accession: A36337
A;Accession: A36337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-918 <HIB>
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                                                                         281
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                                                                                                                                                                                                                                                                                                                                  172 ----CKAKRDTPT-SCTVDY----STVYFVNIEVWVEAENALGKVTSDHINFDPVYKVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 ITIISGLPPEKPKNLSCIVNEG-KKMRCEWDGGRETHLETNFTLKSEWATHKFAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 VHLLVDVPPEEP-QLSCFRKSPLSNVVCEWGP-RST---PSLTTKAVLLVRKFQNSPAED 160
                                                                                                                                                                                                                                                                   217 DPPANITYTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKD---L
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                                                                                                                                    QHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPRAMGTPWTE--SRSP-----PAB
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                NE---
                                                                         RSSFTVQDLKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRPSKAPSFWYKIDPSH 340
                                                                                                                                                                                                       NPPHNLSVINSEELSSILKLTWINPSI--KSVIILKYNIQYRTKDASTWSQIPPEDTAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%; Score 167.5; DB 2; 22.1%; Pred. No. 0.0013; ative 61; Mismatches 133;
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R;Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A;Title: Molecular cloning and characterization of the rat liver
A;Reference number: A44257; MUID:93052397; PMID:1427893
A;Accession: A44257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-6 signal transducing molecule gp130 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: sequence extracted from NCBI backbone (NCBIP:118488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: P40190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-918 <WAN>
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Best Local :
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   528
                                                                     481
                                                                                         446 IITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNAS
                                                                                                                                        451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 VHLLVDVPPEEP-OLSCFRKSPLSNVVCEWGP-RST---PSLTTKAVLLVRKFQNSPAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393
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                                  LLTKLQAQNQW 516
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KVGKNEAVLEW 538
                                                                 LRGSLLESKCYLITVTPVFPGGPGSPESM-
                                                                                                                                      ---KYIL-----EWC----
                                                                                                                                                              KQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVK 445
                                                                                                                                                                                               ASLAARNVVGKSPATVLTIPGSHFKASHPVVDLKAFPKDNLLWVEWTPPSKPVN-----
                                                                                                                                                                                                                                                                  ANHPQEYRSARLIWKTLPLSEANGKILDYEVVLTQSKSVSQTYTVNGTELIVNLTNNRYV
                                                                                                                                                                                                                                                                                                                                      VSPRTSFTVQDLKPFTEYVFRIRSIKENGKGYWSDWSEEASGTTYEDRPSKAPSFWYKVN 336
                                                                                                                                                                                                                                                                                                                                                                       -----HCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTE--SRSP-----
                                                                                                                                                                                                                                                                                                                                                                                                         SPPHNLSVTNSEELSSILKLAW--VNSGLDSILRLKSDIQY---RTKDASTWIQVPLEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCV----ASSVGSKFSKTQTFQGCGILQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITILSGYPPDIPTNLSCIVNEG-KNMLCQLDPGRETYLETNYTLKSEWATEKPPD-----
                                                                                                                                                                                                                                     ----DNILFRDSANATSLP-VEFMPVPPGEDSKDVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----CRTKHGTS--SCMM----GYTPIYFVNIEVWVEAENALGNVSSEPINFDPVDKVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVRNLVGKSDAAVLTIPACDFQATHPVMDLK--AFPKDNMLWVEWTTPRESVKK---YIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NILFRDSANATSLPV-EFMPVPPGEDSKDVAAPHRQPL----TSSERIDKQIRYIL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQGYRTVQLVWKTLPPFEANGKILDYEVTLTRWKSHLQNYTVNATKLTVNLTNDRYLATL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokine receptor homology
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                                                                                                                           ---VLSENSPCIPDWQQEDGTVNR-----
                                                                                                                                                                                                                                                                                                       ----NEVSTPMOALTTNKDD------
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                                                            -KAYLKOAAPSKGPTVRTK 527
                                                                                                                                                                                                                                   ----APHRQPLTSSERID
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prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep_1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
                                                                                          RESULT 28
A29884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Molecule type: protein
A;Notes: the samino end of the mature protein was blocked
C;Keywords: blocked amino end; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-616/Product: prolactin receptor 2 #status predicted <MAT>
F;36-221/Domain: transmembrane #status predicted <MAT>
F;35-258/Domain: transmembrane #status predicted <MAT>
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A;Title: Purification and partial sequence of the rabbit mammary gland prolace, Reference number: A60380; MUID:91146782; PMID:2289615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prolactin receptor 2 precursor - rabbit
N;Alternate names: prolactin receptor, mammary gland
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A30304; A60380
R;Edery, M; JOlicoeur, C; Lievi Meyrueis, C; Dusanter-Fourt, I; Petridou
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A;Title: Identification and sequence analysis of a second form of prolactin
A;Reference number: A30304; MUID:89184578; PMID:2928321
A;Accession: A30304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A60380
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A;Residues: 1-616 <ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent)
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                                                                                                                                                                               EVDDSEDQQLMPAHSKEHSGPGMKP 340
                                                                                                                                                                                                                              PVPPGED-----
                                                                                                                                                                                                                                                                            GYSMVTCIFPP--
                                                                                                                                                                                                                                                                                                            GTPWTESRSPPAENEVSTP-----MQALTTNKDDDNIL-----FRDSANATSLPVBFM
                                                                                                                                                                                                                                                                                                                                                        YLVQVRCKPD--HGFWSVWSPESSIQIFNDFTMKDITVWIFVAVLSTIICLIMVWAVALK 259
                                                                                                                                                                                                                                                                                                                                                                                                             HVVQLRAQEEFGQGEWSEWSPEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEWETHFAGQ-QTQFKILSLYPGQK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R--WLSVTWODPH--SWNSSFYRLRFELRYRAERSKTFTTWMVKDLOHHCVIHDAWSGLR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNSCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTLEVKHPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFSCQLAVPEGDS-SFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPGKPFIFKCRSPEKETFTCWWRPGADGGLPTNYTLTYHK----EGETITHECPDYKTGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPEEPQLSCFRKSPLSNVVÇEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPÇQYSQESQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.6%; Score 161.5; DB 21.8%; Pred. No. 0.002; tive 42; Mismatches 1
                                                                                                                                                                                                          -SKDVAAPHRQP
||::| ;|
                                                                                                                                                                                                                                                                     --VPGPKIKGFDTHLLEKGKSEELLSAFGCQDFPPTADCEDLLVEFL
                                                                                                                                                                                                                           377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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C;Accession: A29884
R;Boutin, J.M.; Jolicoeur, C.; Okamura, H.;
Cell 53, 69-77, 1988
A;Title: Cloning and expression of the rat parameter number: A29884; MUID:88165059;

A; Cross-references: UNIPROT: P05710;

GB:M19304; NID:g206364;

PIDN:AAA41937.1;

PID: g206365

prolactin receptor,
PMID:2832068

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Gagnon,

Edery,

M.; Shirota, M.; Banville,

A; Molecule type: mRNA A; Residues: 1-310 <BOU>

A; Accession: A29884

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A;Cross-references: UNIPROT:P05710; GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390 R;O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A;Title: Differential signal transduction of the short, Nb2, and long prolactin receptor A;Reference number: I55417; MUID:95014432; PMID:7929319
A;Accession: I55417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Jun-1992 #sequence revision 12-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41070; IS417
R;Ali, S: Pellegrini, I: Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
J. Biol. Chem. 266, 20110-20117, 1991
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A41070
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C;Species: Rattus norverier: '"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-412 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-412 < ALI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: A prolactin-dependent immune cell line (Nb2) expresses A;Reference number: A41070; MUID:92041834; PMID:1718958 A;Accession: A41070
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Matches 49; Conserv
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182
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                                       HHC--VIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEA 310
                                                                                                                               PANIT--VTAVARNPRWLSVTWQDP--HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ 274
                                                                                                                                                                                                                     K--FSCQLAVPEGDSS------FYIVSMCVASSVGSKFSKTQTFQGCGILQPDP
                                                                                                                                                                                                                                                                                                           PPEEPOLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K--FSCQLAVPEGDSS------FYIVSMCVASSVGSKFSKTQTFQGCGILQPDP
                                                                                                                                                                           KTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEP
                                                                                                                                                                                                                                                                    PPGKPEIHKCRSPDKETFTCWWNPGTDGGLPTNYSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PANIT -- VTAVARNPRWLSVTWODP -- HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ 274
HQTQFKVFDLYPGQKYLVQTRCKPD--HGYWSRWSQES
                                                                                     PRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HQTQFKVFDLYPGQKYLVQTRCKPD--HGYWSRWSQES 217
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22.5%;
                                                                                                                                                                                                                                                                                                                                                                            5.6%; Score 159; DB 2; 22.5%; Pred. No. 0.0018;
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Pred. No. 0.0012;
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lactogen receptor 1 - rat
(2.Species: Rattus norvegicus (Norway rat)
(2.Species: Rattus norvegicus (Norway rat)
(2.Date: 13.Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
(2.Accession: A34631
(2.Accession: A34631
(3.E.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A,Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA & A;Reference number: A34631; MUID:90241201; PMID:2159291
A,Accession: A34631
A,Accession: A34631
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prolactin receptor 2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Mar-1991 #sequence_revision 28
C;Accession: A36116
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A36116
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A;Residues: 1-610 <ZHA>
A;Residues: 1-610 <ZHA>
A;Cross-references: UNIPROT:P05710; GB:M34083; NID:g205122; PIDN:AAA79273.1; PID:g205123
A;Note: the authors translated the codon GAG for residue 533 as Gly
F;31-216/Domain: cytokine receptor homology <CRS>
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A;Residues: 1-610 <SHI>
A;Cross-references: UNIPROT:P05710; GB:M57668; NID:g206366; PIDN:AAA41938.1; PID:g206367;
F;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Expression of two forms of prolactin receptor in rat
A,Reference number: A36116; MUID:91155948; PMID:2293022
A,Accession: A36116
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, Mol. Endocrinol. 4, 1136-1143, 1990
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     125
                                           219 PANIT--VTAVARNERWISVTWODP--HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ 274
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PRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEVEIRLKPEEAE---EWEIHFTG 181
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22.5%; Pred. No. 0.003;
ative 37; Mismatches 90; Indels
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Pred. No. 0.003;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-630 <SAN>
A;Cross-references: UNIPROT: (91513; GB:L34783; NID:g903846; PID:g903847
F;37-222/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                          C;Accession: I51086
R;Sandra, O.; Sohm, F.; de Luze, A.; Prunet, P.; Edery, M.; Kelly, P.A.
Proc. Natl. Acad. Sci. U.S.A. 92, 6037-6041, 1995
A;Title: Expression cloning of a cDNA encoding a fish prolactin receptor.
A;Reference number: I51086; MUID:95320210; PMID:7597076
A;Accession: I51086
                                                                                                                                                                                                                                                                                                                                 prolactin receptor - Nile tilapia
C;Species: Tilapia nilotica, Oreochromis niloticus
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 33
I51086
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C;Species: Mus mus
C;Species: 02-Aug-19;
C;Accession: 1727/
R;Schoenhaut, D.S
J. Immunol. 148,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I72789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P43432; GB:M86671; NID:g293663; PIDN:AAA39296.1; PID:g293664
                                                                                Matches
                                                                                                   Query Match
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;Species: Mus musculus (house mouse)
;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
;Accession: I72789
                                                                                                 Local
           81 LLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRSTP 140
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                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLRHVVQLRAQEEFGQGEWSEWS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WQDPHSWNS--SFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCPTAEETLPI-ELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ--VEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGNVCVQ--AQDRYYNSSCSKWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEYPDSWSTPHSYFSLKFFVRIQRKKEK-----MKETEEGCNQKGAFLVEKTSTEVQCK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVPEGDSSFYIVSMCVASSVGSKFSKTQT-FQGCGILQPDPPANITVTAVARNPRWLSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKGGETLSHSHLLLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRAGRPAGTVHLLVDVP------PEEPQLSCFRKSPLSNVVCEW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNIKSSSSSPDSRAVTCGMASLSAEKVTL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GPRSTP-----SLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQ--L 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGETVNLTCDTPEEDD---ITWTSDQRHGVIGS-----GKTLTITVKEFLDAGQYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGDSVTLTCPGVEPEDNATVHWV--LRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, 48, 3433-3440, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HQTQFKVFDLYPGQKYLVQTRCKPD--HGYWSRWSQES
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.5%;
                                                                                             21.2%;
                                                                                                              5.5%;
                                                                          52;
                                                                     Score 158; DB
Pred. No. 0.003
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 158.5; DB Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
                                                                                       DB 2;
                                                                       152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113;
                                                                                                                                                                                                                                                                                                                               (Nile tilapia) #text_change 0
                                                                                                      Length 630;
                                                                 Indels 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---DQRDYEKYSVSCQEDV 195
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                                                                                                                                                                                                                                                                                                                                 09-Jul-2004
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                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       м.к.;
prolactin receptor precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence_revision C;Accession: 177524 R;Davis, J.A.; Linzer, D.I.H. Mol. Endocrinol. 3, 674-680, 1989
                                                                                                                  RESULT 35
177524
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F;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 34
177525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-292 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms of the A;Reference number: 157699; MUID:89261824;
A;Accession: 177525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Davis, J.A.; Linzer, D.I.H. Mol. Endocrinol. 3, 674-680,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prolactin receptor precursor - mouse G;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 C;Accession: I77525
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                                                                                                                                                                                                                                                                                                                                                                                                                113 PPEEPQLSCFRKSPLSNTVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQ 172
                                                                                                                                                                                                                                                                                                                          65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 VSMCVASSVGSKFSKTQTFQGCGILQPDPPANITYTAVARNPRW--LSVTWQDPH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 GLPTTYALYYRK----EGSDVVHECPDYHTAGKNSC----FFNKNNTLIWVSYN 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                          HHC--VIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPE 309
                                                                                                                                                                                                                                         PRNLTLEVKQLKDKKTYLWVKWLPPTITDVKTGWFTMEYEIRLKSEEA---DEWEIHFTG 181
                                                                                                                                                                                                                                                                                                                                             K--FSCQLAVPEGDSS------FYIVSMCVASSVGSKFSKTQTFQGCGILQPDP 218
                                                                                                                                                                          HQTQFKVFDLYPGQKYLVQTRCKPD--HGYWSRWGQE
                                                                                                                                                                                                                                                                         PANIT--VTAVARNERWLSVTWODP--HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ
                                                                                                                                                                                                                                                                                                             KNTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEP
                                                                                                                                                                                                                                                                                                                                                                                PPGKPEIHKCRSPDKETFTCWWNPGSDGGLPTNYSL-----TYSKEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSNYEDLLVEYLEVYMPEQQELMVDKGKDHDGCLKS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLTWLIHMNSHSLKHCMLPPVPGPKIKG----FDKQLLKSGKSDEVFSALV--VSDFPPT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCNKSNMCESSKEAL--AENNLNLPKMAEKDGCFQS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGWITLIYELRVKLEDEESEWENHAAGOOKMFNIFSLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITVVATNALGKTYSDPODIDVVYÍVOPHPPEKLEVT-VMKDOGWPFLRVSWEDPRKADTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLPAFVPHTDGTH------YSLPGKPTEIKC-RSPEKETFTCWWKPGSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.4%; Score 155; DB 2; 22.6%; Pred. No. 0.0021; tive 35; Mismatches 91
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                                            02-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the prolactin
4; PMID:2725531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
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                                              09-Jul-2004
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mouse

Gaps

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A;Molecule type: mRNA
A;Residues: 1-557, 'F',559-608 <EDE>
A;Residues: 1-557, 'F',559-608 <EDE>
A;Residues: 1-557, 'F',559-608 <EDE>
A;Cross-references: EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PID:g312697
C;Comment: Prolactin receptor have long form and short form which are result; Comment: This long form receptor is capable of transducing a signal to m:C;Comment: This long form receptor protein
C;Keywords: receptor; transmembrane protein
F;31-216/Domain: cytokine receptor homology <CRS>
F;330-253/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 134, 263-265, 1993
A;Title: Cloning and sequencing of the cDNA encoding the A;Reference number: JT0671; MUID:94085788; PMID:8262385 A;Accession: JT0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G;Species: Mus musculus (house mouse)
G;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
G;Accession: I53289; JT0671; S34356
R;Clarke, D.L.; Linzer, D.I.H.
                                                                                                                                                                                                                                                                                                                                                 A; Accession: S34356
                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S34356
                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L13593; NID:g347398; P.DN:AAC37641.1; PID:g347842 R;Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A. submitted to the EMBL Data Library, June 1993 A;Description: Isolation and nucleotide sequence of a mouse cDNA prolact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-608 < MOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Moore, R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q08501; GB:L14811; NID:g293769; PIDN:AAA02686.1; PID:g293770
R;Moore, R.C.; Oka, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-608 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endocrinology 133, 224-232, 1993
A;Title: Changes in prolactin receptor expression during
A;Reference number: I53269; MUID:93307149; PMID:8319571
A;Accession: I53269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prolactin receptor,
C;Species: Mus muscu
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F;31-216/Domain: cytokine receptor homology <CRS>
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A; Residues: 1-303 < RES>
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                                                                        Query Match
Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PANIT -- VTAVARNPRWLSVTWQDP -- HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ
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                                                                 Score 155; DB
Pred. No. 0.00
35; Mismatches
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5; Mismatches
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A;Cross references: UNIPROT:Q06418; GB:U05682; NID:g463469; PIDN:A R;Ohashi, K.; Mizuno, K.; Kuma, K.; Miyata, T.; Nakamura, T. Oncogene 9, 699-705, 1994
A;Title: Cloning of the cDNA for a novel receptor tyrosine kinase, A;Fatle: Cloning of the cDNA for a novel receptor tyrosine kinase, A;Reference number: JP0077; MUID:94150991; PMID:8108112
A;Accession: JP0077
A;Molecule type: mRNA
A;Fatle: 1-890 <-OHA>
A;Cross-references: DDBJ:D17517; NID:g624880; PIDN:BAA04467.1; PID A;Experimental source: hepatoma HepG2 cell
A;Experimental source: hepatoma HepG2 cell
R;Folvi, A; Armstrong, E; Lai, C.; Lemke, G.; Huebner, K.; Sprit: Gene 134, 289-293, 1993
A;Fitle: The human TYRO3 gene and pseudogene are located in chromota; A;Reference number: JC2145; MUID:94085793; PMID:8262388
A;Accession: JC2145
A;Molecule type: mRNA
A;PG1-700 - DD7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 519-790 <POL>
A;Residues: 519-790 <POL>
A;Crose-references: EMBL:X72886; NID:g296020; PIDN:CAA51396.1;
R;POlvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Al submitted to the EMBL Data Library, March 1993
A;Description: Human Tyro3 gene and pseudogene in chromosome 1f A;Reference number: S32219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine kinase (EC 2.7.1.112) tyro3 precursor - human N;Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase (Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A53743; JP0077; JC2145; S32765; S32219 R;Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J. J. Biol. Chem. 269, 10720-10728, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: rse, a novel receptor-type tyrosine kinase with A;Reference number: A53743; MUID:94193774; PMID:7511603 A;Accession: A53743
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A; Residues: 1-890 < MAR>
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Down syndrome cell adhesion protein 1 - human (fragment)
N;Alternate names: Down syndrome cell adhesion molecule
N;Alternate names: Down syndrome cell adhesion molecule
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T08851
R;Yamakawa, K.; Huo, Y.K.; Haendel, M.A.; Hubert, R.; Chen, X.N.; Lyons, G.E.; Korer
submitted to the EMBL Data Library, September 1997
A;Description: DSCAM: A novel member of the immunoglobulin superfamily maps in a down, Reference number: Z16495
A;Accession: T08851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:AF023449; NID:93169765; PID:93169766
A;Cross-references: EMBL:AF023449; NID:93169765; PID:93169766
A;Experimental source: brain; developmental stage: 14 weeks; fetal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGLLLAALASLLLPESAAAGLKLMGAPVKLTVSQGQPVKLNC-SVEGMEEPDIQWVKDGA
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                                                                                                  FSNGSFIIRTVKAEDSGYYSCIANNNWGSDEIILNLQVQVPPDQPRLT-VSKTTSSSITL 138:
                                                                                                                                ----LLLRSVQLHDSGNYSCY---RAGRPAGTVHLLVDVPPEEPQLSCFRKSFLSNVVC 132
 VPEGDSSFYIVSMCVASSVGS--KFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVT 237
                                   SWLPGDNGGSSIRGYILQYSEDNSEQWGSFPISPSER----SYRLENLKCGTWYKFTLT 1438
                                                                    EWGPRSTPSLTTKAVLLVRKFQN-----
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                                                                                                                                                                                                                                                                                                                                                     from alternately-spliced mRNA
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                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                    in nervous system development splicing
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                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                      Score 144; DB 2; E pred. No. 0.15; 9; Mismatches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLLRDLVPATNYSLRVRCANALGPSPYADWVP
                                                                        -SPAEDFQEPCQYSQESQK----FSCQLA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119;
                                                                                                                                                                                                                                                                        Length 1896;
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RESULT 39
B59405
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_ch
C;Accession: B59405; B49400
R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
J. Biol. Chem. 276, 41086-41094, 2001
J. Biol. Chem. 859405; MUID:21538812; PMID:11518703
A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: B59405
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A;Reference number: B49400
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <HTZ>
A;Residues: 1-288 <HTZ>
A;Residues: 1-288 <HTZ>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (S1a and S1b) of the human proactin receptor 96 ta-casein gene promoter activation, with S1b more effective than S1a. However, their ligs
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A; Residues: 1-288 < HU1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: glycoprotein; transmembrane protein F;1-24/Domain: signal sequence #status predicted <SIG>F;25-288/Product: prolactin receptor, short form S1b #:F;25-288/Product: prolactin receptor homology <CRS>F;36-221/Domain: cytokine receptor homology <CRS>F;59,104,233/Binding site: carbohydrate (Asn) (covalen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Keywords: glycoprotein; transmembrane pro
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A; Gene: GDB: PRLR
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submitted to GenBank, December, 1999
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prolactin receptor short form Sla precursor, breast cancer cells C;Species: Homo sapiens (man) C;Date: 01-Peb-2002 #sequence_revision 01-Peb-2002 #text_change 0 C;Accession: A59405; A49400
                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WODPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG---CAEKQANFATLNYDGSTIPPLIKSVVQNEEGLTTNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQES 171
                                                                                                                                                                                                                                                                                                                                                                                                                                         LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHR-
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                                                                                                                                                                                                                                                                                                        ANITYTAVARNER--WLSVTWODEH--SWNSSEYRLREELRYRAERSKTETTWWV-----
                                                                                                                                                                                                                    ----KDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSP
                                                                                                                                                                                                                                                                LELAVEVKOPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKA---AEWEIHFAGO 187
                                                                                                                                                                             QTEFKILSLH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.8%;
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                                                                                                                                                                                  -PGQKYLVQVRCKPD--HGYWSAWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 138; DB 2; Pred. No. 0.031; 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    ---FYIVSMCVASSVGSKFSKTQTFQGCGILQPDPP
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#text\_change 09-Jul-2004

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Search completed: December Job time : 51.8543 secs
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A;Map position: 5p13.3-5p13.1
C;Keywords: glycoption; transmembrane protein
C;Keywords: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-376/Product: prolactin receptor, short form S1a #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
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J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin recept A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: A59405
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C;Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor eta-casein gene promoter activation, with S1a less effective than S1b. However, their lited COS-1 and HEX293 cells is due to rapid intracellular turnover of the receptor. #expe
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A;Molecule type: DNA
A;Residues: 1-376 <HU2>
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A; Accession: A49400
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A; Residues: 1-376 < HUl>
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Best Local S
Matches 49
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nes 49; Conserv
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                                                                                                                        188 QTEFKILSLH---
                                                                                                                                                                                                                                                131 LELAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKA---AEWEIHFAGQ 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 VPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQES 171
                                                                                                                                                                                                                                                                                                                                                                     71 LMHECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHR-----EGET 70
                                                                                                                                                                                                                                                                                                                                                                                                                              QKFSCQLAVPEGDSS-----FYIVSMCVASSVGSKFSKTQTFQGCGILQPDPP 219
                                                                                                                                                                              ----KDLOHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.8%; Score 138; DB 2; Length 376; llarity 22.1%; Pred. No. 0.044; Conservative 32; Mismatches 89; Indels
                               9, 2004, 09:21:49
                                                                                                                        ----PGQKYLVQVRCKPD--HGYWSAWSP 220
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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O9tth4 aotus nigri
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Q2819 phoca vitul
O95181 equus cabal
O28747 orcinus orc
O9xt80 delphinapte
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O865x6 lama glama
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P26893 sus scrofa
P41683 felis silve
O97535 aotus vocifi
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O18796 sus scrofa
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P05231 homo sapien
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Tanaka Y., Waki M., T cell or ripheral blood cernative splicing  AND DISULFIDE BONDS. S., Reid G.E., sites of the f receptor.";	nanishi Y., Seed B.,  1(1988).  Hirano T.,  hepatic interleukin-6 in HepG2 cells.";	anishi Y., Seed B., n-6 (BSF-2/IFN beta 2)	L-6R-alpha) (IL-6R 1) ata; Euteleostomi; idae; Homo.		P26892 bos taurus P29455 ovis aries Q6v919 bubalus bub Aaq54301 bubalus b O35736 marmota mon Q9jhh3 marmota mon Q6uan5 tetraodon n Aar25684 tetraodon P26607 rattus norv Q9mzr1 oryctolagus Q91213 sigmodon hi P08505 mus musculu Q9wyq8 mesocricetul Q9wyi0 gallus gall

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EMBL; X12830; CAAA31312.1; -.

REMBL; X58298; CAAA41331.1; -.

REMBL; X58298; AAC60635.1; -.

REMBL; S73848; AAC60635.1; -.

REMBL; S7384; AAC60635.1; -.

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Taga T., Kishimoto T.;
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Varghese J.N., Moritz R.L., Lou M.-Z., Van Donkelaar A.,
Ivancic N., Branson K.M., Hall N.E., Simpson R.J.;
"Structure of the extracellular domains of the human into
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                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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-TISSUE SPECIFICITY: Isoform 2 is expressed in peripheral blood
-TISSUE SPECIFICITY: Isoform 2 is expressed in peripheral blood
-TISSUE SPECIFICITY: Isoform 2 is expressed in peripheral blood
-TISSUE SPECIFICITY: Isoform 2 is expressed in peripheral blood
-TISSUE SPECIFICITY: Isoform 2 is expressed in peripheral in urine and serum.
-TISSUE SPECIFICITY: Isoform together a cytokine-binding domain.
-TISSUE SPECIFICITY: The WSWS motif appears to be necessary for proper protein
-DOMAIN: The WSWS motif appears to be necessary for proper and cell-
-BOMAIN: The WSWS motif appears to be necessary for protein
-Folding and thereby efficient intracellular transport and cell-
-SUMIACCE receptor binding.
-TISSUE SPECIFICITY: Selongs to the type I cytokine family of receptors.
-SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eptor alpha-chain.";
c. Natl. Acad. Sci. U.S.A. 99:15959-15964 (2002).
puNCTION: Part of the receptor for interleukin 6. Binds to IL-6
puNCTION: Part of the receptor for interleukin 6. Binds to IL-6
with low affinity, but does not transduce a signal. Signal
with low affinity, but does not transduce a signal. Signal
activation necessitate an association with IL6ST. Activation may
activation necessitate an association with IL6ST. Activation may
lead to the regulation of the immune response, acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reactions and hematopoiesis.

FUNCTION: Low concentration of a soluble form of interleukin-6 receptor acts as an agonist of IL6 activity.

SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST.

SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).

Secreted (isoform 2).

Secreted PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1; Synonyms=Long;
IsoId=P08887-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Subfamily 3.
SIMILARITY: Contains 1 fibronectin type III domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
DATABASE: NAME=PROW; NOTE=CD guide CD126 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd126.htm".
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335; IG_LIKE; 1.
Alternative splicing; Direct protein sequencing;
Alternative splicing; Receptor; Signal; Transmembrane.
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Cytoplasmic (Potential).

Ig-like C2-type.

Fibromectin type-III.

WSXWS motif.
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N-linked (GlcNAc.
N-linked (GlcNAc.
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Extracellular
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C-yA: Complete loss of ligand-binding.

W-yL: Complete loss of ligand-binding.

P-yG: No change of ligand-binding and
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C->S: Complete loss
F->A: No change of 1
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C->L: Comp
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D->T: 30% decrease
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C->D: Complete loss of ligand-binding
C->A: No change of ligand-binding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F->L: NO
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V->N: 50% Decrease of ligand-binding (50% increase in IL6 signaling.
1.>D: Complete loss of ligand-binding.
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                                                                       no IL6 signaling.
Q->K: Complete loss
R->G: Complete loss
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G->D: 80% decrease
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                Name=IL6R;
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                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed in liver.
DOMAIN: The two fibronectin type III-like domains
C-terminal part form together a cytokine-binding companies.
DOMAIN: The WSXWS motif appears to be necessary for
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                                                                                                                                                    Matteri R.L.;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003530; HemptreceptL_F3.
InterPro; IPR007110; Ig-like.
Pfam; pF00041; fn3; 1.
Pfam; pF00047; ig; 1.
Pfam; PF00047; ig; 1.
PROSITE; PS50853; FN3; 1.
PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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surface receptor binding.
SIMILARITY: Belongs to
Subfamily 3.
SIMILARITY: Contains 1
SIMILARITY: Contains 1
                       301
                                                                                                    241
                                                                                                                                          181
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AF015116; AAB70916.1;
P08887; 1N26.
                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                  VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                                                                                 PHSWNSSFYRLRFELRYRAERSKTFTTWWVKDLQHHCVIHDAWSGLRHVVQLRAQEBFGQ
                                                                                                                                                                      PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                   CFRKSPLSNVGCEWRPRSPPSPTTKAVLLVRKFQNSPVEDFQEPCQYSLEAQRFFCQLAV
                                                                                                                                                                                                                                                                                                             VLRNQVTGSPDGRPAGVGRRLLLKSVQLSDSGNYSCYQDGVPAGSVRLLVDAPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                            MLAVGCALLTALLAAPGMALAPRGCSKLEVAQDVLTSLPGASVTLTCPGGEPGDNATIHW
                                                             PPSWNSYFYRLQFELRYRAERSKTFTTWMVKELQHHCIIHDAWSGMRHVVQLRAQBEFGH
                                                                                                                                             PEGDNSFHIVTLCVANSAGSQSSTPQTFEGYGILQPDPPVNITVSAVDRNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002996; Cytkn_recept_B/G.
IPR003961; FN_III.
IPR008957; FN_III-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.3%;
75.1%;
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1 immunoglobulin-like C2-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig-like C2-type.

Ig-like C2-type.

Fibronectin type-III.

WSXWS motif.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlcNAc...

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1468;
Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGA RAT STANDARI
P22273;
01-AUG-1991 (Rel. 19, 0
01-FEB-1995 (Rel. 31, 1
05-JUL-2004 (Rel. 44, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Fischer 344; TISSUE=Liver; STRAIN=Fischer 346; PubMed=2174054; MEDLINE=91060602; PubMed=2174054; Baumann M., Baumann H., Fey G.H.; Molecular cloning, characterization "Molecular cloning, characterization"; rat liver interleukin 6 receptor "; rat liver interleukin 6 receptor "; J. Biol. Chem. 265:19853-19862(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                              InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN III
InterPro; IPR003967; FN III-like.
InterPro; IPR003530; Hemptrecepti_F3.
InterPro; IPR003530; Hemptrecepti_F3.
InterPro; IPR007110; Ig-like.
Pfam; PF00041; fn3; 1.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished observations (FEB-1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DENTIFICATION OF PROBABLE FRAMESHIFT
                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation its European Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics Institutions as long as its content is in no way use by non-profit institutions as long as its content is no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                RGD; 2902;
InterPro; I
InterPro; I
                                                                                                                                                                                HSSP;
RGD;
                                                                                                                                                                                          EMBL; M58587; AAA41431.1; --
PIR; A37986; A37986.
HSSP; P08887; 1N26.
                 PROSITE; PS50853; FN3; 1.
PROSITE; PS50354; HEMATOPO REC_L_F3;
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with low affinity, but does not transduce a signal Signal with low affinity, but does not transduce a signal Signal activation necessitate an association with IL6ST Activation activation necessitate an association with El6ST acute-phase lead to the regulation of the immune response, acute-phase reactions and hematopoiesis.

SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
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                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
SUBCELIULAR LOCATION: Type I membrane protein.
SUBCELIULAR LOCATION: Type I III-like domains contained in the DOMAIN: The two fibronectin type III-like domains contained in the C-terminal part form together a cytokine-binding domain.
C-terminal part form together a cytokine-binding domain.
C-terminal part form together a cytokine-binding for proper protein DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
SIMILARITY: Belongs to the type I cytokine family of receptors.
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 fibronectin type III domain. SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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        Immunoglobulin
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Rodentia;
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Last annotation updat
or alpha chain precurso
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Sciurognathi; Muridae; Murinae; Rattus.
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                domain;
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precursor
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                   Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IL-6R-alpha)
                     signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL6R and IL6ST
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RESULT 4
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AC MARMEN
AC STRAIN
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RX SUGITA
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DOMAIN
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DISULFID
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CONFLICT
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                                                                                                                                          TIGA MOUSE STANDARD; PRT; 460 AA.
P22272;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-6 receptor alpha chain precursor
Name=Il6ra; Synonyms=Il6r;
                                                                                             Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPRKNPLVNAFCEWHPSSTPSPTTKAVMFAKKINTINGKSDFQVPCQYSQQLKSFSCEVE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ppeswopsyyllofelryrpvwskxftvwplqvaQHqcvlHbalrgvxHvVdvrgkeefd
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                                                                                                                                                                                                                                                                                                                                                                                                                   QGEWSEWSPRAMGTPW-TESRSPPAENEVSTRMQALTTNKDDDNILFRDSANATSL--PV
                                                                                                                                                                                                                                                                                                                          QGSSPIP
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                                                                                                                                  (Mouse)
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462
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385
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408
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                                                                                                      Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig-like C2-type
Fibronectin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 991; DB
Pred. No. 2.3e
51; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A4D6064CEDC0537D CRC64;
                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type-III.
                                                                                                                                                                                                                                                          460
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.3e-61;
                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112;
                                                                                                                  Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 462;
                                                                                                                                                                             (IL-6R-alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                         Euteleostomi;
; Murinae; Mus
                                                                                                                    Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                      (IL-6R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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(1)
SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Spleen;
STRAINE-90278354; PubMed=2112585;
MEDLINE-90278354; PubMed
MEDLINE-90278354; PubMed
Totsuka T., Saito M.,

Yamasaki

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Taga

Hirano

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Query
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DOMAIN
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PROSITE;
PROSITE;
                                     CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                      CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X51975; CAA36237.1; -.

EMBL; X53802; CAA37810.1; -.

PIR; JL0144; JL0144.

PIR; JL0145; JL0145.

HSSP; P08887; 1N26.
                                                                                                                                                                                                                                                Glycoprotein; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fiorillo M.T., Ciliberto Submitted (JUL-1990) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C3H; TISSUE
                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    particle gene product at its plasmacytomagenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:105304; Il6ra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kishimoto T.; "Functional murine interleukin 6 receptor with the intracisternal "Functional murine interleukin 6 receptor with the intracisternal particle gene product at its cytoplasmic domain. Its possible role
                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                             nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: The two fibronectin type III-like domains contained in the C-terminal part form together a cytokine-binding domain.

DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

SIMILARITY: Belongs to the type I cytokine family of receptors. SUMILARITY: Contains 1 fibronectin type III domain.

SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
with low affinity, but does not transduce a signal. Signal
activation necessitate an association with IL6ST. Activation may
lead to the regulation of the immune response, acute-phase
reactions and hematopoiesis.
SUBUNIT: Haramar for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reactions and hematopoie SUBUNIT: Hexamer of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
                                                                                                                                                                                                                                                                                                            PF00041; fn3; PF00047; ig;
                                                                                                                                                                                                                                                                        PS50853; FN3; 1.
PS01354; HEMATOPO_REC_L_F3;
PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                 IPR002996; Cytkn recept_B/G.
IPR003961; FN_III.
IPR008957; FN_III-like.
IPR003530; HemptreceptL_F3.
                                        171:2001-2009(1990)
                                                                                                                                                                                                                                                             Immunoglobulin
                                       33.4%;
                          ž
                                   POLY-Pro.
WSXMS motif.
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N-linked (GlcNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecules each of IL6,
                                                                                                                                                                                            Potential Cytoplasm
                                                                                                                                                                                                                                                         domain; Receptor; Signal; Transmembrane.
 Score
                                                                                                                                                               Ig-like C2-type.
Fibronectin type-III.
                                                                                                                                                                                                                      Extracellular (Potential)
                                                                                                                                                                                                                                   Interleukin-6
 954.5;
                                                                                                                                                                                              lasmic (Potential).
 BB
                                                                                                                                                                                                                                  receptor alpha
1;
                          CRC64;
 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IL6R and IL6ST
                                                (Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
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RESULT TRESULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=87067433; PubMed=3538015;
May L.T., Helfgott D.C., Sebigal P.B.;
May L.T., Helfgott D.C., Sebigal P.B.;
"Anti-beta-interferon antibodies inhibit the increased e:
"Anti-beta-interferon antibodies inhibit the increased e:
"Anti-beta-interferon antibodies inhibit the increased e:
"Anti-beta-interferon involved.";
structural studies of the beta 2 interferon involved.";
structural Acad. Sci. U.S.A. 83:8957-8961(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL6 HUMAN
SIMILARY
P05231; Q9UCU2; Q9UCU3; Q9UCU4;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
-----leukin-6 precursor (IL-6) (B-cell stimulatory (TL-6) (B-cell stimulatory (TL-6))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=87065033; PubMed=3491322;
Hirano T., Yasukawa K., Harada H., Taga T., Watanabe
Kashiwamura S.-I., Nakajina K., Koyama K., Iwamatsu
Sakiyama F., Matsui H., Takahara Y., Taniguchi T., K
"Complementary DNA for a novel human interleukin (BS
B lymphocytes to produce immunoglobulin.";
Nature 324:73-76(1986).
                                                                                                                                                                                                                                                                                        "Structure and 2/IL-6) gene.";
                                                                                                                                                                                                                                                                                                                                          Nakai S., Kishimoto
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88082664; PubMed=3500852;
Yasukawa K., Hirano T., Watanabe Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=IL6; Synonyms=IF
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                gene.";
6:2939-2945(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LAPVQESSSMSLP
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RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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MEDLINE=87053818; PubMed=3023045;

Zilberstein A., Ruggieri R., Korn J.H., Revel M.;

"structure and expression of cDNA and genes for human interferon-beta-
"structure and expression of cDNA and genes for human interferon-beta-
2, a distinct species inducible by growth-stimulatory cytokines.";
2, a distinct species inducible by growth-stimulatory cytokines.";
2, a distinct species inducible by growth-stimulatory cytokines.";
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J. Immunol. 139:4116-4121(1987)
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Tonouchi N., Miwa K., Karasuyama H., Matt
"Deletion of 3' untranslated region of hu
stabilization of the mRNA and high-level
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MEDLINE=87004683; PubMed=3758081;
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Chung-Hua Chung Liu Te
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FHCRC, Seattle, WA
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Witek-Giannotti J., Hewick
ukin 6: identification as a
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, de Groot E.R.,
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sa Chih 14:340-344(1992)
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n of human BSF-2 m
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hematopoietic
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W., Lee K.L.,
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J databases.
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colony-stimulating
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MEDLINE=88154445;
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MEDLINE=91355644; PubMed=1883960;
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  MEDLINE=97224126; pubMed=9118960;
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EMBO J. 16:989-997(1997).

FUNCTION: IL-6 is a cytokine with a widd
-1- FUNCTION: IL-6 is a cytokine with a widd
of B-cells into Ig-secreting cells, it:
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                                                                                                                                                                                                "Folding topologies of human interleukin-6 an y NMR spectroscopy."; slochemistry 35:273-281(1996).
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Beeumen J., Decock
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anabe A., Gouda H.,
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RX MEDLINGEZCAT7999; PubMed=12853948;
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RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McCherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Caresky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Crandia C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spleth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis B.R.,
RA Clifton S.W., Chisses S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Boxk P., Suyama M.,
Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler B.E., Green E.D.,
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Mammalia; Eutheria;
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PTM: N- and O-glycosylated.

SIMILARITY: Belongs to the IL-6 superfamily.

DATABASE: NAME=R&D Systems' cytokine mini-reviews: IL6;

WWWW-"http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=208".
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Pred. No. 4e-58;
0; Mismatches
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                    354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
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Query Match
Best Local Similarity
Matches 187; Conserv
              Query Match
Best Local :
                                                                   SEQUENCE FROM N.A.

Ebert L., Schick M., Neubert P., Schat

"Cloning of human full open reading fi

"cloning of human full open reading fi

vector (pDONR201).";

vector (pDONR201).";

charted (MAY-2004) to the EMBL/GenBe

EMBL; CR450296; CAG2992.1;

NON_TER 212 212
                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pu
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                            CAG29292;
CAG29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 424:157-164(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. SECUENCE 212 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2004) to the EMBL; AC073072; AAS07539.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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Submitted
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                                                                                                                                                                                                                                                    IL6 protein
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20-MAY-2004
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Submitted (JUN-2000)
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              Similarity
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(SEP-2001)
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                                                       212 AA;
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Primates;
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sapiens BAC clone RP11-;
to the EMBL/GenBank/DDBJ
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Pred. No. 4e
              Score 938.5;
Pred. No. 4e-
                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                         1F1ED1FE1B734079 CRC64;
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                                                                                                                            Schatten R.,
ing frames in
                                                                                                                                                                                                                                                                                 sequence update)
                                                                                                                                                                                                                                                                                                                            212
              4e-58;
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Gateway(TM)
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  Indels
                                                                                                                                           Korn
                              212;
                                                                                                                             system
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RESULT 8
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P79341;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
7nterleukin-6 precursor (IL-6)
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL6_MACFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning
                                                                                                               PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PTCDOm; PD004356; Interleukin_6;
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6;
                                             DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                  InterPro; IPR009079; 4_hellx_cytokine.
InterPro; IPR003573; II6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                         HSSP;
                                                                                CHAIN
                                                                                              SIGNAL
                                                                                                         Acute
                                                                                                                                                                            Pfam; PF00489; IL6;
                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                               FUNCTION: IL-6 is a cytokine with a wide variety of biological functions; it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity). SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142
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                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                        AB000554; BAA19148.1; -. P05231; 1IL6.
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72
101
73
172
212
                                        ; Cytokine; (29) 1 29 30 212 78 78 111 111 73 73 172 172
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                           ΑA,
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                                                                                                                       INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212
                         e; GlycopTotein; Growth factor; S
29
By similarity.
11
By similarity.
11
By similarity.
11
N-linked (GleNAc. . .) (1)
72
N-linked (GleNAc. . .) (2)
23654 MW; CF8173FCBF0B0389 CRC64
                            23654 MW;
      31.7%;
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        Score
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        907.5;
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Matches 181; Conserv
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P51494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
05-UU1-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae;
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interleukin-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96003435; PubMed=7561102;
Villinger F.J., Brar S.S., Mayne A.E., Chil
"Comparative sequence analysis of cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=RAC 2;
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its ture by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonhuman primates."
                                                                                                                                                                                                         EMBL; L26028; AAA99978.1; -.
HSSP; P05231; 1ALU
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
InterPro; IPR003574; Interleukin_6.
IPR00489; II6; 1.
                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                       PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PRODOM; PD004356; Interleukin_6;
                            SIGNAL
                                                                                                SMART; SM00126; II
PROSITE; PS00254;
                                                                       Acute phase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: IL-6 is a cytokine with a wide variety of biologica functions: it plays an essential role in the final differenti of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, plasmacytoms growth, it induces nerve cells differentiation, hepatocytes it induces acute phase reactants (By similarity). SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Belongs to the IL-6 superfamily.
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                                                                                                                          SM00126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor (IL-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                         Cytokine; Glycoprotein;
            1
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72
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                                                                                                                            IL6;
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                                                                                                           INTERLEUKIN_6; 1.
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3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
               By similarity.
Interleukin-6.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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There are no restrictions on its
There are no restrictions on its
long as its content is in no way
moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                         Growth
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kine genes from human
                                                                                                factor;
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Best Local
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097540; 01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2004 (TrEMBLrel. 26,
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification, cloning, and sequencing of differ in four species of owl monkey.";
Immunogenetics 54.645-653(2002).

EMBL; AF014510; AAD01536.1; -...
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005128; F:interleukin-6 receptor binding;
GO; GO:000518; F:immune response; IEA.
                                                                                                                                                                                                                                                           PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aotus nancymaae (Ma's night monkey).
Eukaryota; Metazoa; Chordata; Craniata; Ve;
Mammalia; Eutheria; Primates; Platyrrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=IL-6;
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murillo L.A., Patarroyo M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22354194; PubMed=12466897;
Hernandez E.C., Suarez C.F., Mende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                        Similarity
                               LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
                                                                                                                                                                                                                                  PS00254; INTERLEUKIN_6; 1.
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WPAAFPAPVPPGEDSKEVAAPNRQPLTSTEQIDKHIRYILDGISALRKETCNKSNMCESS
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                                                                                                                                                                                                                                                                                                                                                                IPR009079; 4 helix_cytokine.
IPR003573; IL6_MGF_GCSF.
IPR003574; Interleukin_6.
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larity 94.7%;
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N-inked (GlCNAc...) (Potential).
N-linked (GlCNAc...) (Potential).
4130DFE0CF0BCCAD CRC64;
                                                                                 Score 898.5; DB 2;
Pred. No. 2.6e-55;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mendez J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 899.5; DB
Pred. No. 2.2e-59
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ni; Cebidae; Aotinae; Aotu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 1;
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                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Immunol. 155:3946-3954 (1995).

-i- FUNCTION: IL-6 is a cytokine with a wide variety of biologics functions: it plays an essential role in the final differenti of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, hepatocytes it induces acute phase reactants.

-i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96003435; PubMed=7561102;
Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
"Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P46650;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                        SEQUENCE
                                                                                                                                                                PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD004356; Interleukin
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBJ
                                                                                                                          SIGNAL
                                                                                                                                                                                                                 InterPro; IPR003574; Interleukin 6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nonhuman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Cercocebus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-6 precursor (IL-6).
                                                                                                                                       Acute phase; Cytokine;
                                                                                                                                                     PROSITE; PS00254;
                                                                                                                                                                                                                                               InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR003573; IL6_MGF_GCSF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the IL-6 superfamily.
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                                                                   29
212
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111
73
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 31.3%;
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                                         MW;
                                                   By similarity.
Interleukin-6.
By similarity.
By similarity.
N-linked (GlcNAc...
N-linked (GlcNAc...
 Score
Pred.
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No.
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                                         CRC64;
              Length
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Best Local Similarity

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413

82

Matches

178;

Conservative

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Mismatches

7;

Indels

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142 473

RESULT Q8MKH0

12

Q8MKH0 Q8MKH0;

PRELIMINARY;

PRT;

212

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01-OCT-2002 01-OCT-2002 01-MAR-2004

(TrEMBLrel.) (TrEMBLrel.

22, 26,

Created)

Last sequence update)
Last annotation update)

Interleukin-6. Saimiri sciureus (Common squirrel monkey). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;

밁 Š

> 202 533

LOSSLRALROM

212

LOSSLRALROM 543

212

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354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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                                                                                           KEALAENNIAULPKWAEKDGCFOSGENEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
                       avomštkgi i ostorkakni saiatė bėatnaši i tri daopomiog vithi i ir sėkė ė
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Cebinae; Saimiri.
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Murillo L.A.; Patarroyo M.E.;
Infentification, cloning, and sequencing of
"Identification, cloning, and sequencing
in four species of owl monkey.";
in four species of owl monkey.";
in four species of owl monkey.";
in four species of owl monkey.";
in four species of owl monkey.";
in munogenetics 54:645-63 (2002).

EMBL; AP097223; AP721298.1; --:
IDAC, GO:0005125; F:cytckine areceptor bit
GO; GO:0005125; F:cytckine response; IEA.
GO; GO:0005125; F:inmune response; IEA.
R privrs; PR00433; ILGGCSPMG.
R PRIVRS; PR00433; ILGGCSPMG.
R PRIVRS; PR00434; INTEXLEUKIN.6; 1.
R PROSITE; PS00126; ILG; 1.
R PROSITE; PS00126; INTEXLEUKIN.6; 1.
R PROSITE; PS00126; INTEXLEUKIN.6; 1.
R PROSITE; PS00126; INTEXLEUKIN.6; 1.
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Matches 162
RESULT
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AC Q9
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01-MAY-2000 (TrEMBLrel. 1:
01-MAR-2004 (TrEMBLrel. 2:
01-MAR-2004 (TrEMBLrel. 2:
Interleukin-6 (Fragment).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
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SEQUENCE FROM N.A.

MEDLINE=22354194; PubMed=12466897;

Hernandez E.C., Suarez C.F., Mendez J.A.,

Murillo L.A., Patarroyo M.E.;

Murillo L.A., Patarroyo M.E.;
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   01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAR-2004 (TrEMBLrel. 26, La
Interleukin-6 (Fragment).
Namel-6;
Aortica
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SEQUENCE
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Q9TTH4;
Q1-MAY-2000
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01-MAR-2004
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 Aotus nigriceps
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162; Conserv
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209 AA;
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                                                                              PRELIMINARY;
     (Black-headed
                                                                                                                                                      540
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23115 MW; A0A3DFAA4BF560CC CRC64;
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86.2%; Pred. No. 2.
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Last sequence update)
Last annotation updat
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Aotinae; Aotu
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"MOLECULAR CONTROL OF BEING CO. GO: 00005125; P.

GO; GO: 00005.75; P.

GO; GO: 00005.75; P.

C. M. A. PubMed=11976788; Arrayla M.; Aranji M.; Arandar cipning, characterization, and "Molecular cipning, characterization, and "Molecular cipning, characterization, and monkey ( Saimiri sciureus) Thi and Th2 cyt monkey ( Saimiri sciureus) Thi and Th2 cyt RT Immunogenetics 54:20-29(2002).

BR EMBL; AR\$294757; AAK\$2044.1; -.

DR GO; GO:0005125; P.

GO; GO:0005125; P.

GO; GO:0005125; P.

GO; GO:0005125; P.

and quantification yetokines.";

GO; GO:0005125; F:cytckine activity; IEA.
GO; GO:0005125; F:cytckine activity; IEA.
GO; GO:0005125; F:interleukin-6 receptor binding; IEA.
GO; GO:0005138; F:interleukin-6 receptor
GO; GO:0006955; P:immune response; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0006957; III MOF GCSF.
IIIterPro; IPR003573; III MOF GCSF.
IIIterPro; IPR003574; Interleukin\_6.
PRINTS; PR00434; INTERLEUKING.
PRINTS; PR00434; INTERLEUKING.

ProDom; PD004356; Interleukin\_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN\_6; 1.
SEQUENCE 212 AA; 23581 MM; FF722CBF493245479 CRC64;

Ş 밁 á

413

Query Match Best Local S Matches 163

Similarity

28.0%;

; Score 801.5; I ; Pred. No. 1.8e. 9; Mismatches

8e-48;

DB 2; 18;

Length Indels

Conservative

В

82

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LOSSLRALROM

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Best Local Similarity
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                  Youn H. Y., Shin I.-S.;
Submitted (JUN-2000) to the EMBL/GenBank/DDI
Submitted (JUN-2000) to the EMBL/GenBank/DDI
EMBL; AP7275796; AFF86275.1; -.
HSSP; P05231; IIL6.
GO; GO:0005175; F:cytrokine activity; IEA.
GO; GO:0005125; F:interleukin-6 receptor bi:
GO; GO:0005135; F:interleukin-6 receptor bi:
GO; GO:0005135; F:interleukin-6 receptor bi:
GO; GO:0006357; Interleukin-6.
InterPro; IPR003574; Interleukin-6.
Pfam; PF00489; IL6; 1.
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01-OCT-2000
01-MAR-2004
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InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                     Wallie-12 (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Wallia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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PRINTS; PR00433; IL6GCSPMGF.
PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD004356; Interleukin 6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenetics 54:645-653(2002).

EMBL; AF097322; AAF21297.1; -.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005125; F:cytokine activity; IEA.

GO; GO:0005138; F:interleukin-6 receptor binding; IEA.

GO; GO:0005138; P:immune response; IEA.
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MEDLINE=22354194; PubMed=12466897;
Hernandez E.C., Suarez C.F., Mende
Murillo L.A., Patarroyo M.E.;
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9MYZ7;
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NON_TER 1 1
SEQUENCE 175 AA; 19205 MW; 2BCC
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=IL-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-6.
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Mammalia; Eutheria;
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     IL6GCSFMGF
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26,
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Pred. No. 1.3e
10; Mismatches
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Last sequence up
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nes 13;
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Matches 116
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SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
SEQUENCE 207 AA; 23042 MW; 4554
                                                                                                                                                                                                                                                                                                                                                                                            IL6 PHOVI STANDARD; PRT; 209 AA. (28819) 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stott J.L., Ferrick D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96163018; PubMed=8575817;
King D.P., Schrenzel M.D., McKnight M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phoca vitulina (Harbor seal).
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P05231;
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                                                                                                                                            AAB01430.1; -.
1IL6.
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Pred. No. 1.1e-3
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(See http://www.isb-sib.
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orca), and
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Pfam; PF00489; II PRINTS; PR00433; PRINTS; PR00434;

IL6;

INTERLEUKIN6 IL6GCSFMGF InterPro; IPR009079; 4 helix\_cytokine. InterPro; IPR003573; II6\_MGF\_GCSF. InterPro; IPR003574; Interleukin\_6.

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Jon; pD004356; Int.
JART; SM00126; IL6; 1.
PROSITE; PS00254; INT.
KW Acute phase; Cytr.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                 Eguus caballus (Horse).
Eguus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-6 precursor
                                                                                                                                                                                                                                                                         MEDLINE=20579380; PubMed=11137120;
Swiderski C.E., Sobol G., Lunn D.P.,
"Molecular cloning, sequencing, and (
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9796;
                                                                                                                                                                               Leutenegger C.M., Huder "Molecular cloning of eq submitted (JUL-1997) to [3]
                                            "Cloning and expression of equine interleukin-6.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: It-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).

hepatocytes it induces acute phase reactants (By similarity).

-i- SUBCELLULAR LOCATION: Secreted.

-i- SUBCELLULAR LOCATION: Secreted.
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      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation the the Swiss Institute of Bioinformatics are no restrictions on its European Bioinformatics Institute. There are no restrictions on
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Cytokine; Glycoprotein; Growth
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By similarity.
By 51714922E43B48E9 C
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pred. No. 1.7e-32;
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ProDom; PD004356; Interleukin_6;
SWART; SM00126; IL6; 1.
PROSITE; PS00754
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use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (Secon send an email to license@isb-sib.ch).
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EMBL; AF005227; AAB62246.1; ---
EMBL; AF041975; AAC04574.1; ---
EMBL; T09216; T09216.
HSSP; P05231; 1ALU.
HSSP; P05231; 1ALU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
PRINTS; PR00433; IL6GCSFMGF.
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Q28747;
30-MAY-2000 (R
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Interleukin-6
SEQUENCE FROM N.A.

MEDLINE=96163018; PubMed=8575817;

MEDLINE=96163018; PubMed=8575817;

King D.P., Schrenzel M.D., McKnight

King D.P., Schrenzel M.D.A.;

Stott J.L., Ferrick D.A.;

"Molecular cloning and sequencing of
                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                             Orcinus
                                                       NCBI_TaxID=9733;
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                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                          (Rel.
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                                                                                                                Rel. 39, Created)
Rel. 39, Last sequence update)
Rel. 44, Last annotation update)
precursor (IL-6) (Fragment).
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23325
                                                                                                                                                                STANDARD;
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Cetartiodactyla; Cetacea; Odontoceti; Delphin
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Interleukin-6.
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N-linked (GlcNAC....
LS -> FF (in Ref. 3).
T -> A (in Ref. 3).
I -> V (in Ref. 3).
V -> I (in Ref. 3).
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Pred. No. 2.8e-32;
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I -> V (in Ref. 2).
V -> I (in Ref. 3).
V -> I (in Ref. 3).
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InterPro; IPR003573; II6 MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
PRINTS; PR00433; IL6GCSFWGF.
PRINTS; PR00434; INTERLEUKIN6.
PRODDom; PD004356; Interleukin_6; 1.
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Delphinapterus leucas (Beluga whale).
Delphinapterus leucas (Beluga whale).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
Monodontidae; Delphinapterus.
NCBI_TaxID=9749;
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PROSITE; PS00254; INTERLEUKIN_6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
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ea otter (Enhydra lutris nereis).";
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Interpro; IPR003573; II6_MGF_GCSF.
Interpro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
PRINTS; PR00433; II6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN 6.
PRODOm; PD004356; Interleukin_6; 1.
SMART; SM00126; II6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
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"Molecular cloning, phylogenetic analysis and expression of whale (Delphinapterus leucas) interleukin 6.";

Vet. Immunol. Immunopathol. 73:31-44(2000).

EMBL; AP076643; AAD42929.1; -.

HSSP; P05231; 1ALU.
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                                                                                   STRAILNEMONGRE1;
MEDLINE=94303924; PubMed=7913298;
MEDLINE=94303924; PubMed=7913298;
Kukislka G.L., Youker K.A., Hawkins H.K.,
Ballantyne C.M., Smith C.W., Entman M.L.;
"Regulation of ICAM-1 and IL-6 in myocard:
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Mammalia; Eutheria; Carnivora;
MCBI_TaxID=9615;
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Canis familiaris (Dog).
Chordata; Craniata; Vertebrata; Euteleostomi;
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GO:0005125; P:cytokine activity; IEA.
GO:0005138; F:interleukin-6 receptor
GO:0006955; P:immune response; IEA.
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                                  . N. Y. Acad. Sci. 723:258-270(1994).

FUNCTION: IL-6 is a cytokine with a wide variety of biologics functions: it plays an essential role in the final differention of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, hepatocytes it induces acute phase reactants.
           SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.A.
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Pred. No. 1.3e-31;
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81CC85C6E80389C4
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                                                                                                                                                                                           of biological
                                                                                                                                                    differentiation
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U12234; AAA83030.1; -. HSSP; P05231; 1IL6.
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DISULFID
SEQUENCE
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PRINTS; PR00434; INTERLEUKIN6.
PTCDOm; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                 LAMGL
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CHAIN
                                                                                                                                                                                                                               IL6_LAMGL
Q865X6;
29-MAR-2004
29-MAR-2004
  Onuma M.;
"Cloning and sequence analysis of cytokine cDNAs of llama and camel.";
"Cloning and sequence analysis of cytokine cDNAs of llama and camel.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

In FUNCTION: II-6 is a cytokine with a wide variety of biological
-!- FUNCTION: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
plasmacytoma growth, it induces nerve cells differentiation, in
plasmacytoma growth, it induces nerve cells differentiation, in
plasmacytoma growth, it induces nerve cells differentiation.
                                                                                                                                                                           Lama glama (Llama).
                                                                                                     Raadan
                                                                                                                 SEQUENCE
                                                                                                                                        NCBI_TaxID=9844;
                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                         Interleukin-6
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 of B-cells in
plasmacytoma
hepatocytes i
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114; Conserv
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                                                                                                   0., Lee
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67
96
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(Rel. 43,
(Rel. 44,
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                                                                                                                                                                                                          precursor
                                                                                                                                                                                                                                                                         STANDARD;
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22945 MW;
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                                                                                                         Yoshida R.,
                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Tylopoda; Camelidae; Lama.
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                             (IL-6).
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By similarity.
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No. 1
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RESULT 22
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ID Q865W
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Best Local S
Matches 109
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is no modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUNCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
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PROSITE; PS00254; INTERLEUKIN_6; 1.
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PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                              Q865W7;
Q865W7;
01-JUN-2003
01-JUN-2003
01-MAR-2004
Onuma M.;

Submitted (APR-2003) to the EMBL/GenBank/DDBJ data Submitted (APR-2003) to the EMBL/GenBank/DDBJ data Submitted (APR-2003) to the EMBL/GenBank/DDBJ data EMBL; AB107656; BAC75393.1;

HSSP; P05231; 1116.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005125; F:cytokine activity; IEA.

GO; GO:0005138; F:interleukin-6 receptor binding;
                                                                                                                                 Camelus bactrianus (Bactrian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
                                                                                                                    NCBI_TaxID=9837;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                    Interleukin
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DFLQFSLRAVRIM
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211 AA;
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77 B:
110 B:
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56.5%;
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24, Last sequence update)
26, Last annotation updat
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Pred. No. 2.5e
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bh factor; Signal By similarity. Interleukin-6.
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By similarity.
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                                                                                          R.,
                                                                                                                                                                                                                                                      PRT;
                                                                                            Chang
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                                                                                              Ohashi K.,
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InterPro; nterPro;

GO:0006955; P:immune response; IEA.

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Matches
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PRINTS; PR00433; IL6GCSPMGF.

PRINTS; PR00435; INTERLEUKIN6.

PRODOm; PD004356; Interleukin_6; 1.

SMART; SM00126; IL6; 1.

PROSITE; PS00544; INTERLEUKIN 6; 1.

PROSITE; PS00544; INTERLEUKIN 6; 1.

SEQUENCE 211 AA; 23929 MW; ODF800
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
28-FEB-2003 (Rel. 41, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
Interleukin-6 precursor (IL-6).
"Cloning and expression of interleukin 6 gene from Landrance x Meishan hybrid swine.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: II-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                           Mathialagan N., Bixby J.A., Roberts M.R. "Expression of interleukin-6 in porcine, preimplantation conceptuses."; preimplantation conceptuses."; Mol. Reprod. Dev. 32:324-330(1992).
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Landrace x Meishan; TISSUE=Blood;
Liu S., Meng M., Gao R.;
                                                                                                                                                                                                                                                                                        Richards C., Saklatvala J.;
"Molecular cloning and sequence of porcine expression of mRNA in synovial fibroblasts
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=91338547; PubMed=1873476;
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                              Name=IL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL6 PIG
P26893; Q95KN6;
                                                                                                                                                                                                                                   MEDLINE=92360284; PubMed=1497880;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            Cytokine 3:269-276(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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Local Similarity 57.0%;
nes 110; Conservative 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR009079; 4 helix cytokine.
IPR003573; IL6 MGF GCSF.
IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Pred. No. 2.5e
34; Mismatches
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actyla; Suina; Suidae;
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in vitro.";
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Sus.
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InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
PRINTS; PR00433; II6GCSFMGF.
PRINTS; PR00433; INTERLEUKING.
PRODOm; PD004356; Interleukin_6; 1.
SWART; SM00126; II6; 1.
                                                                                                                                                                                                                                                                         Q8MJ75
Q8MJ75;
01-OCT-2002
01-OCT-2002
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DISULFID
DISULFID
CONFLICT
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SIGNAL
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SEQUENCE FROM N.A.
Lee D., Yoo H., Choi I.;
Submitted (JUN-2002) to the EMBL,
EMBL; AF518322; AAM74938.1; -.
HSSP; P05231; 1ALU.
GO; GO:0005576; C:extracellular;
                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M86722; AAC37333.1; -.
EMBL; M80258; AAC27127.1; -.
EMBL; AF309651; AAG27730.1; -.
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Acute phase; Cytokine; Glycoproteir
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PIR; I46621; I46621.
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212
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                                                                                                                                                                     Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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57.5%;
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Interleukin-6.
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E -> G (in Ref.
                                                                EMBL/GenBank/DDBJ
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Pred. No. 2.8
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                                                                  databases
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Sus.
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GO:0006955; P:immune response; IEA.

R IntearPro; IPR009079; 4 helix cytokine.

R IntearPro; IPR003574; II.6 MGF-GCSF.

R PINTEO; IPR003574; Intearleukin_6.

R PERNYTS; PR0043; II.6; 1.

R PRINTS; PR0043; INTERLEUKIN6.

R PRINTS; PR0043; INTERLEUKIN6.

R PRODOM; PD004356; Intearleukin_6; 1.

R SMART; SM00126; II.6; 1.

R SMART; SM00126; II.7 ERLEUKIN_6; 1.

R SMART; SM00126; INTERLEUKIN_6; 1.
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Matches 111
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p41683;
p41683;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
01-NOV-1995 (Rel. 44, Last annotation
Interleukin-6 precursor (IL-6).
                                                                                                                                                                                                                                                                                 Pelis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                        Hasegawa A.; "Molecular cloning
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=94162386;
                                                                                                                                                                                                                                                                    NCBI_TaxID=9685;
                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Lymphocytes;
MEDLINE=94052249; PubMed=8234373;
MEDLINE=94052249; PubMed=8234373;
Bradley W.G., Gibbs C., Kraus L., Good F
WMolecular cloning and characterization
                                                                                                                                                                                                                               Ohashi T., Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0005125; F:cytokine activity; IEA.
GO:0005138; F:interleukin-6 receptor binding; IEA.
GO:0006955; P:immune response; IEA.
                                                                                                                      interleukin-6.";
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||:| || || ||:| | : :: :: |:||| |||:|:| ||
                              PUNCTION: IL-6 is a cytokine with a wide variety of biological FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.

SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Belongs to the IL-6 superfamily.
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   SWISS-PROT entry
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                                                                                                                                                                                                                                PubMed=8117820;
oto Y., Watari T.,
                                                                                                                                                                                                   55:941-944(1993).
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                                                                                                                                                                                                            of feline interleukin-6
        Institute
    is copyright. It is produced through a collaboration stitute of Bioinformatics and the EMBL outstation -
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Pred. No. 3.8e
33; Mismatches
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Felis.
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                                                                                                                                              feline
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Query Match
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Matches 107
the Buropean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L16914; AAA16620.1; --
EMBL; D13227; BAA02507.1; --
EMBL; I46084. I46084.
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Pfam; PF00489; IL6GCSPMGF.
PRINTS; PR00433; INTERLEUKING.
PRINTS; PR00434; Interleukin_
ProDom; PD004356; Interleukin_
SMART; SM00126; IL6; 1.
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PROSITE; PS00254; INTER
Acute phase; Cytokine;
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InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
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DISULFID
CONFLICT
CONFLICT
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                                                                                                                                                         097535 PRELIMINARY;
097535; (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, I
01-MAR-2004 (TrEMBLrel. 26, I
01-MAR-2004 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
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                                                                                                        Aotus vociferans (Spix's owl monkey).
Aotus vociferans (Spix's owl monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                              Name=IL-6;
 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-22354194; PubMed=12466897;

MEDLINE-22354194; PubMed=2 C.F., Mendez

Murillo L.A., Patarroyo M.E.;

Murillo L.A., Patarroyo M.E.;

"Identification, cloning, and sequer

"Identification of owl monkey.";

in four species of owl monkey.";
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nilarity 55.4%;
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68
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133
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74
107
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133
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Interleukin-6.
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Ref. 2).
FS -> LR (in Ref. 2
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Pred. No. 2.2e
33; Mismatches
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Last sequence update)
Last annotation update)
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           sequencing
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                                                 J.A.,
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Aotinae; Aotu
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Best Local Sin
Matches 107;
                                                                                                                                                                                                     EMBL; I46804; AAB01428.1; -...
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005126; F:cytokine activity; IEA.
GO; GO:0005128; F:interleukin-6 receptor bi.
GO; GO:0005955; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PP00489; II6; 1.
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Q28403;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2004
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PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
NON_TER 1
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor
GO; GO:000555; P:immune response; IEA.
GO; GO:0006955; P:immune response; IEA.
                           ProDom; PD004356; Interleukin_6; SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and sequencing of interleukin 6 cDNA the harbor seal (Phoca vitulina), killer whale (Orcinus Southern sea otter (Enhydra lutris nereis)."; Immunogenetics 43:190-195(1996).
EMBL; L46804; AAB01428.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enhydra lutris (Sea otter).
Eukaryota; Metazoa; Chordata;
                                                                                                                                      PRINTS; PRO0433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Stott J.L., Ferrick D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enhydra
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InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVOMSTK 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                       INTERLEUKIN_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carnivora;
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0; Mismatches
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Pred. No. 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07A021338650A46D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fissipedia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi; ia; Mustelidae; Lutrinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5e-30;
9;
                                                                                                                                                                                                                                                                                                                                                                                                           binding;
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Best Local S
Matches 104
                                                                                                                                                    Query Match
Best Local
                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8MKE5;
01-OCT-2002
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                      PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PRODOM; PD004356; Interleukin_6; 1.
SMART; SM00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
SEQUENCE 214 AA; 23765 MW; 5084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                             InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; II6_MGF_CCSF.
InterPro; IPR003574; InterPeukin_6.
Pfam; PF00489; II6; 1.
                                                                                                                                                                                                                                                                                                                                                          Wu M. Gao R. Li J. Meng M.,
Submitted (MAR-2002) to the EM
EMBL; AF493992; AAM27192-1; --
HSSP; P05231; 1ALU
                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8MKE5
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
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                                                             408 MCESSKEALAENNINIPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESS
                                                                                                                   351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
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                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAFPT---PGPLGGDSKDDATSNRPPLTSADKMEDFIKFILGKISALRNEMCDKYNKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCE
                      EEQARAVOMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQ
                                                                                             ATAPPT----PGRLEEDAKGDATSDKMLFTSPDKTEELIKYILGKISAMRKEMCEKYE
                                                                                                                  ATSLPVEFMPVPPG---EDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFLOFSLRAIRIM 207
 KGNVEAVQISTKALIQTLRQKGKNPDKATTPNPTTNAGLLDKLQSQNEWMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHSVYISTKHLLOTL--RPMNQIEVTTPDPTTDASLQALFKSODKWLKHTTIHLILRRLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                   17.5%;
57.3%;
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e EMBL/GenBank/DDBJ
                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                          Score 501.5; DB 2
Pred. No. 2.5e-27;
8; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 516.5;
Pred. No. 2.1
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J databases
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RESULT

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Best Local :
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05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                        AAS73282;
AAS73282;
29-MAR-2004
29-MAR-2004
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NON TER
SEQUENCE
SEQUENCE FROM N.A.
O'Brien R., Berger S., Griffin F.;
"Cervine interleukin-6 gene.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY540191; AAS73282.1; -.
NON_TER 1
                                                                                                                                                                                                                    Cervus elaphus (Red deer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Brien R., Berger S., Griffin F.;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ
EMBL; AYS40191; AAS732821; -
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; IT6_MGF_GCSF.
InterPro; IPR003573; IT6_MGF_GCSF.
InterPro; IPR003573; Interleukin_6.
Pfam; PF00489; IL6; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
Cervinae; Cervus.
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Cervus elaphus (Red deer).
                                                                                                                                                                                                                                                                                     Interleukin-6 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                  Cervinae; Cervus.
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                                                                                                                                                                    NCBI_TaxID=9860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
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SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENFLQFSLRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKEFLOSSLRA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENVKDLRSSIRTLLQIMRQ--KSIDLVTT--ATTNPDLLEKMQSSNEWVKNAKIILILRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HISTORY AMASAFPT---PGPLGEDFKNDTTPSRLLLTTPDKTEALIKHIVDKISAMRKEICEKNDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CENSKETLAENNLNLPKMKEKDGCFQSGFNQETCLIRSTVGLLEYQTYLDYLQNEYEGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191
191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.9%;
49.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21677 MW;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 482.5; DB 2;
Pred. No. 4.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                      Euteleostomi;
cora; Cervidae;
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IL6_CAPHI
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Best Local Similarity
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01-NOV-1997
01-NOV-1997
05-JUL-2004
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SEQUENCE
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EWBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97392354; PubMed=9250586;
Takakura H., Mori Y., Tatsumi M.;
"Molecular cloning of caprine IL-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                               PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PRO0434; INTEXLEUKIN
PRODOM; PD004356; Interleukin
SMART; SM00126; IL6; 1
                                                                                                                                                                                                                                                        EMBL; D86569; BAA13118.1; -. HSSP; P05231; 1IL6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=11
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Acute phase;
                             PROSITE; PS00254;
                                                                                                                                                      Pfam; PF00489; IL6; 1
                                                                                                                                                                      InterPro; IPR003573;
InterPro; IPR003574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL6 CAPHI
                                                                                                                                                                                                                              InterPro; IPR009079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RINCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiat of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, ir hepatocytes it induces acute phase reactants.

SUBCELULUAR LOCATION: Secreted.

SIMILARITY: Belongs to the IL-6 superfamily.
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191
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(Rel. 35, Last sequence up
(Rel. 44, Last annotation
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  Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (IL-6).
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                             INTERLEUKIN_6; 1.
                                                                       Interleukin_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21677 MW;
                                                                                                                                                                            4 helix cytokine.
IL6 MGF GCSF.
Interleukin 6.
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49.7%; Pred. No. 4.6e-26;
Glycoprotein; Growth
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       factor;
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  Signal.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ULT 32
BOVIN
                                                                                                                                                                                                            MEDINE-3076003; PubMed=1446077;
MEDINE-3076003; PubMed=1446077;
Proogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
Mucleotide sequence of bovine interleukin-6 cDNA.";

NA Seq. 2:411-413(1992).

-I- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.

-I- SUBCELLULAR LOCATION: Secreted.
-I- SIMILARITY: Belongs to the IL-6 superfamily.
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DISULFID
CARBOHYD
SEQUENCE
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL6_BOVIN STANDARD;
P26892;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seq
05-JUL-2004 (Rel. 44, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                         EMBL; X57317; CAA40572.1; PIR; A56610; A56610.
                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                STRAIN-Holstein;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=IL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin-6
    P05231; IIL6.
P05231; IIL6.
Pro; IPR009079; 4 helix cytokine.
rPro; IPR003573; II6_MGF_GCSF.
rPro; IPR003574; Interleukin_6.
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    Last sequence update)
    Last annotation updat

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Interleukin-6.
By similarity.
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Matches 94
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CARBOHYD
                                            modified
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MEDLINE=94041419; Barcham G.J., Ashma
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SMART; SM00126; IL6;
PROSITE; PS00254; IN
                                                                     between the Swiss Institute or Browner the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Ebrahimi B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA."
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Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                mmunol.
                                                                                                                                                                 FUNCTION: II-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity). SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Belongs to the II-6 superfamily.
                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.D.;
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non-profit institutions as long as its content is in and this statement is not removed. Usage by and for comrequires a license agreement (See http://www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IR
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-6 precursor (IL-6).
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Interleukin-6.
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N-linked (GlCNAC...
W; A0F000B9BA2EC341 (
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Pred. No. 3.4e-25;
""matches 51;
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                                                                                                      and the
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EMBL; X68723; CAA48662.1; -.
EMBL; A19159; CAA01443.1; -.
EMBL; X62949; S116.1; -.
EMBL; X
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Premraj A., Sreekumar E., Rasool T.J.;
Submitted (JUL-2003) to the EMBL/GenBank
EMBL; AY347710; AAQ54301.1;
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
InterPro; IPR003574; Interleukin_6.
PERINTS; PR00434; INTERLEUKIN6.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                Bovinae; Bubalus.
NCBI_TaxID=89462;
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X68723; CAA48662.1; -.
A19159; CAA01443.1; -.
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(TrEMBLrel. 27, Last ann
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L - R (in Ref. 2).
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he EMBL/GenBank/DDBJ
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SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6;
SEQUENCE 208 AA; 23772 MW; 00
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AAQ54301;
02-MAR-2004
02-MAR-2004
02-MAR-2004
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bubalus.
N(BI_TaxID=89462;
                                                                                                                                                                                                                                                                                    Premraj A., Sreekumar E., Rasool T.J.;
"Identification and molecular characterization of major
"Identification and molecular characterization of major
of Indian water buffalo (Bubalus bubalis).";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX347710; AAQ54301.1;
SEQUENCE 208 AA; 23772 MW; 0C3F0374C52E7342 CRC64;
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Matches 88
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InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN.6; 1.
PRODOm; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y14139; CAA74571.1; -. HSSP; P05231; 1ALU.
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MEDLINE=98139533; PubMed=9472070;
Lohrengel B., Lu M., Roggendorf M.;
"Molecular cloning of the woodchuck cytokines: TNF-alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marmota monax (Woodchuck)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentia of B-cells into Ig-secreting cells, it induces myeloma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmacytoma growth, it induces nerve cells differentiation, hepatocytes it induces acute phase reactants (By similarity). SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the IL-6 superfamily.
193
                                                 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phase; Cytokine; Glycoprotein; Growth factor; Signal.
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                                                 FKEFLOSSLRALRO 542
                                                                                                         DRAEHVOSSSKALIEILKQEVKDPNKIVFPSPTANINLLAKLESQNDWQKVMTMQLILSN
                                                                                                                                                     ARA---VQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRS
                                                                                                                                                                                                             KSHVAVSENNLNLPKYTEKDGCFQTGYNRDDCLVRITSGLLEFQVYLRYIRNKFQEGNNR
                                                                                                                                                                                                                                           SSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQ
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(Rel. 38, Last sequence update)
(Rel. 44, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                          15.3%; Score 437.5; DB 1;
larity 45.4%; Pred. No. 7.7e-23;
Conservative 39; Mismatches 62;
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By similarity.
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Interleukin-6.
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Matches
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GG; GG:00055125; F:cytokine activity; IEA.
GG; GG:0005138; F:interleukin-6 receptor binding; IEA.
GG; GG:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; IL6_MGF_GGSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
PFAMINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00433; INTERLEUKIN.6.
                                                                                                                                                                                                                 Query Match
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Hepatology 34:1049-1059(2001).

EMBL; AF012908; AAF34861.1; -.

EMBL; AF122896; AAF28873.1; -.

EMBL; AF333966; AAK52717.1; -.

HSSP; P05231; IALU.
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01-OCT-2000
05-JUL-2004
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Оэлннз;
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Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Rodent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Augmented hepatic interferon gamma expression and T-cell influx characterize acute hepatitis progressing to recovery and residualifelong virus persistence in experimental adult woodchuck hepati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Li D.H., Cullen J.M.;
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Peripheral blood;
Li D.H., Cullen J.M.;
Submitted (JUL-1997) to
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                 ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21536769; PubMed=11679978;
Hodgson P.D., Michalak T.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                        411 SSKEALAENNINLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQ
193
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                                                          ARA---VQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRS
                                                                                             KSHVAVSENNLNLPKMTEKDGCFQTGYNRDNCLVRITSGLLEFQVYLRYIRNKFQEGNNR
                                                                                                                                                                   ATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCE
                                                                                                                                             ATAFPASELQREDGENSVTRNKPTR---ASSGKTAGQISYLIKEVFEMRKELCKNDETCI
FEDFLQFTLRAVRK
                     FKEFLOSSLRALRO 542
                                             DRAEHVQFSSKALIETLKQEVKDPNKİVFPSPTANINLLAKLESQNDWQKVMTMQLILSN
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Rodentia;
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                                                                                                                                                                                                      Score 435.5;
Pred. No. 1.1
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Sciurognathi;
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thi; Sciuridae; Sciurinae;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence

05-JUL-2004 (TrEMBLrel. 27, Last annotati

05-JUL-2004 (TrEMBLrel. 27, Last annotati

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Class I helical cytokine receptor number
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ARR25684;
Q2-MAR-2004 (TrEMBLrel. 27, Last sequence update)
Q2-MAR-2004 (TrEMBLrel. 27, Last amoutation update)
Q2-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Class I helical cytokine receptor number 21.
Class I helical cytokine receptor number 21.
CRPA21.
CRPA21.
Tetraodon nigroviridis (Green puffer).
CRPA21.
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Cranitata; Euteleosteni;
Eukaryota; Neopterygii; Teleosteni; Euteleosteni;
Eukaryota; Neopterygii; Percomorpha; Tetraodontiformes;
Actinopterygii; Neopterygii; Percomorpha; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodon
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pred. No. 6.7e-20;
pred. No. 131;
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submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; A2374493; AAR25684.1;
Receptor.
SEQUENCE 528 AA; 59805 MW; AlOA8F86391B198C CRC64;
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"Tetraodon nigroviridis
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JOUL-2004 (Rel. 44, Last annotation update)

Interleukin-6 precursor (IL-6).

Name=Il6; Synonyms=Il-6;
Rattus norvedicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Murinae; Rat
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                        J. Biol. Chem. 264:16072-16082(1989).

J. Biol. Chem. 264:16072-16082(1989).

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J. Biol. Chem. 264:16082(1989).

J. Biol. Chem. 
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MEDLINE=89380206; pubMed=2789217;
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Pfam; PF00489; IL6; 1.

R PRINTS; PR00433; IL6GCSFMGF.

R PRINTS; PR00434; INTERLEUKIN.6; 1.

R PROOM; PD004356; Interleukin.6; 1.

JR SMART; SM00126; IL6; 1.

JR SMART; SM00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN.6; 1.

PR PROSITE; PS00254; INTERLEUKIN.6; 1.

THE SIGNAL 1 24 Potential.

PT SIGNAL 1 25 211 Interleukin.6.

PT CHAIN 25 211 Interleukin.6.

PT DISULFID 70 76 By similarity.

PT DISULFID 99 109 By similarity.

PT DISULFID 99 109 By similarity.
Search completed: December 9, 2004, 09:20:54 Job time : 252.038 secs
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EMBL; M26745; AAA41430.1; -.

PIR; A34247; A34247

HSSP; P05231; IALU.

RGD; 2901; I16.

InterPro; IPR009079; 4 helix cytokine.

InterPro; IPR003573; II6_MGF_GCSF.

InterPro; IPR003574; Interleukin_6.

Pfam; PF00489; IL6; 1.
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                                                                  530 KEFLQSSLRALRQ 542
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198 EEFLKVTMRSTRQ 210
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Maximum Match 100%
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 Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being put and is derived by analysis of the total score distribution.
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## ALIGNMENTS

transcription regulator, ROK family Atu4567 [imported] - Agrobacterium tumefaciens (strai C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004 C;Accession: AC3118 R;Accession: AC3118 C; Raul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellat, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

ster, E.W. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AC3118

A;Status: preliminary

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.

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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D98169
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-402 <KUR>
A;Cross-references: UNIPROT:Q8U787; GB:AB007870; PIDN:AAK88878.1; PID:g15158645; GSPDB:Gr C;Genetics:
A;Gene: AGR L_609
A;Map position: linear chromosome
                                                                                                                                                                                                                         R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quro. A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-382 <KUR>
A;Cross-references: UNIPROT:Q8U787; GB:AE008689; PIDN:AAL45361.1; PID:g17743056; GSPDB:GNA;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                        frcR protein (AF196574) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: D98169
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A;Map position: linear chromosome
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Pred. No.
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; Lappas, C.; Markelz, B.;
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-405,'A',407-1171 <ARN>
A; Residues: 1-405,'A',407-1171 <ARN>
A; Residues: 1-405,'A',407-1171 <ARN>
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A; Cross-reference number: 35503; MUID:93247479; PMID:8483412
A; Reference number: 35503; MUID:93247479; PMID:8483412
A; Reference number: 35503; MUID:93247479; PMID:8483412
A; Rolecule type: DNA
A; Rolecule type: DNA
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A; Rolecule type: DNA
A; Rolecule type: DNA
A; Cross-references: EMBL:XI3109
A; Cross-references: EMBL:XI3109
A; Cross-references: EMBL:XI3109
A; Note: the authors translated the codon ATT for residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
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A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for Residue 28 a
A; Note: the authors translated the codon ATT for Residue 27 as Tyr, TAC for Residue 27 as Tyr, T
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C.Date: 25-Feb-1985 #sequence revision 12-Apr-1996 #text change 09-Jul-2004
C.Accession: S01997; S01836; 335903; S21414; A04461; S36-947
C.Accession: S01997; Buchanan-Wollaston, V.; Ally, D.; Ally, A.; Beynon, R.; Cannon, M.; Cannon, F.; Buchanan-Wollaston, V.; Ally, D.; Ally, A.; Beynon, R.; Title: The nucleotide sequence of the nifJ gene of Klebsiella pneumoniae.
A; Title: The nucleotide sequence of the nifJ gene of Klebsiella pneumoniae.
A; Reference number: S01997; MUID:89083580; PMID:3060860
A; Reference number: S01997; MUID:89083580; PMID:3060860
A; Status: translation not shown
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C;Species: Klebsiella pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1171 < CAN>
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Best Local
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A; Residues: 1-127 <SHE>
A; Cross-references: GB:X01007;
C; Genetics:
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Nucleic Acids Res. 11, 4241-4250, 1983
A;Title: An open reading frame upstream from the nifH gene
A;Reference number: A04461; MUID:83246546; PMID:6306580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-127,129-135,'S',137-153,'TI',160,'IST',161-169 <
A;Cross-references: EMBL:X16345; NID:g43864; PIDN:CAA34396.1;
A;Cross-references: EMBL:X16345; NID:g43864; PIDN:CAA34396.1;
                                                                                                                              A;Description: transfers one electron from pyruvate to flavodoxin
A;Pathway: nitrogen fixation
C;Superfamily: pyruvate (flavodoxin) dehydrogenase; ferredoxin 2[4Fe-4S] homology
C;Superfamily: pyruvate (flavodoxin) dehydrogenase; protein; metalloprotein; oxidoreducta
C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein; oxidoreducta
C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein; oxidoreducta
F;684-763)Domain: ferredoxin 2[4Fe-4S] homology <FER>
F;691,694,697,755/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F;701,745,748,751/Binding site: 4Fe-4S cluster (Cys) (covalent)
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C; Function:
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8; Conserv
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| Similarity
8; Conserv
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    Conservative
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80.0%;
                                                  68.7%;
72.7%;
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        ; Score 46; DB; Pred. No. 11; 2; Mismatches
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                                                                                                     Length 1171;
                             Indels
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hypothetical protein - Deinococcus radiodurans (strain R1)
c;Species: Deinococcus radiodurans
c;Species: Deinococcus radiodurans
c;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
c;Accession: B75290
C;Accession: B75290
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do
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S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Science 286, 1571-1577, 1999
A;Title: Genome agquence of the radioresistant bacterium A;Title: Genome agquence of the radioresistant bacterium A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome A;Title: Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome Genome G
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A; Residues: 1-396 < WHI>
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E71491
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A;Title: Genome sequence of an obligate intracellular pathogen A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71491
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A;Cross-references: UNIPROT:O84633; GB:AE001333; GB:AE001273; NID:g3329068; PIDN:AAC6823;
A;Experimental source: serotype D, strain UM-3/Cx
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Accession: B75290
White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, White, O.; Eisen, J.A.; Lam, P.; McDonald, Chan M.; Vamathevan, J.J.; Lam, C.M.
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Best Local S
probable membrane protein YOR079c - yeast (Saccharo N;Alternate names: hypothetical protein O2960 C;Species: Saccharomyces cerevisiae C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 C;Accession: S66962
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S66962
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8; Conserv
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pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41;
Pred. No.
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                                                              #text_change 09-Jul-2004
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                                                                                                                                                                       cerevisiae)
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T.; Zalewski,
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RESULT 8
S56206
                                                   C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S56206
C;Accession: Natiou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma,
R;Murakami, Y.; Natiou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma,
submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                 A; Reference number: A; Accession: S56206
                                                                                                                                                  probable membrane protein YFL049w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
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A; Reference number: A82950;
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A; Residues: 1-313 < BOH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-347 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S66962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S66929
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Matches 7
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: UNIPROT:Q916G8; GB:AE004470; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            robable binding protein component of ABC transporter PA0323 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;294-310/Domain: transmembrane
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
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50; MUID:20437337; PMID:10984043
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Pred. No. 23;
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Pred. No.
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A.; Larbig,
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K.; Lim,
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Matches
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70668
A;Accession: C70668
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DMA: A;Cross-references: UNIPROT:P96289; GB:Z83858; GB:AL123456; NID:g3261675; PIDN:CA;Experimental source: strain H37Rv
C;Genetics:
A;Gene: mmpL7
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C;Keywords: transmembrane protein
F;121-137/Domain: transmembrane #/
                                                                                                                                    A;Cross-references: UNIPROT:Q55309; EMBL:M84476; NID:g154543; IC;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase
C;Keywords: cysteine biosynthesis; oxidoreductase; sulfotransfi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphoadenyly1-sulfate reductase (thioredoxin) (EC 1.8.4.8) - Syneo N;Alternate names: 3'-phosphoadenyly1sulfate reductase, thioredoxin N;Contains: 3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (C;Species: Synechococcus sp. C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #s
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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A;Residues: 1-623 <MUR>
A;Cross-references: UNIPROT:P43554; EMBL:D50617; NID:g836685; PID:d1009830; PID:g836706;
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S28609
C;Accession: S28609
C;Accession: A; Gisselmann, G.; Schwenn, J.D.
R;Niehaus, A.; Gisselmann, G.; Schwenn, J.D.
Plant Mol. Biol. 20, 1179-1183, 1992
Plant Mol. Biol. 20, 1179-1183, 1992
A;Title: Primary structure of the Synechococcus PCC 7942
A;Title: Primary structure of the Synechococcus PCC 7942
A;Title: Primary structure of the Synechococcus PCC 7942
A;Title: Primary structure of the Synechococcus PCC 7942
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                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-232 < NIE>
                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S28609; MUID:93099269; A; Accession: S28609
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Pred. No.
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87471
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A87471
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protein F5J5.15 (imported] - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 C;Accession: B86483 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sensory box/GGDEF family protein VC2370 [imported] - Vibrio cholerae (strain N16961 sero
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A; Residues: 1-492 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-579 <HEI>
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                                                                                                                                          B86483
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Best Local (
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8; Conserv
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77.8%;
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Pred. No. 48;
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0; Mismatches
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Pred. No.
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             Federspiel, N.A.; Kaul,
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                                                                 #text_change 09-Jul-2004
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                     White,
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                     Alonso,
                   C;Accession: C64658
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R;Tomb, J.F.; White, D.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McFeterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McFeson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey san, J. Santhays, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID:97394467; PMID:9252185
A; Accession: C64658
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C64658
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                                                                                                                                                                                                                                                                             outer membrane protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.: C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano; H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Ritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Recession: B86481; MUID:21016719; PMID:11130712
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A;Cross-references: UNIPROT:Q9SKV5; GB:AE005172; NID:g6598587; PIDN:AAF18642.1; GSPDB:GNC
C;Genetics:
                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9ZKA5; GB:AE001531; GB:AE001439; NID:g4155617; PIDN:AAD0661:
A;Experimental source: strain J99
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathor, Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: E71857
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable outer membrane protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb_1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
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7; Conserve
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GFGVVLGGKFV
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Pred. No. 1.5e
3; Mismatches
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Pred. No.
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1.5e+02
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Smith, H.O.; Fraser,

C.>

A.; McKenney Watthey, L.

R.D.,

A; Molecule type: DNA A; Residues: 1-230 < TOM>

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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, DNA, Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Ae A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72521
                                                                                                                                                                                                                                                                                   R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: H81685
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H81685
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A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-308 < TET>
                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein TC0598 [imported] - Chlamydia muridarum (strain C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81685
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A; Residues: 1-274 < KAW>
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C;Species: Aeropyrum pernix
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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Best Local S
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                  FGAGLILG 112
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63.6%;
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Pred. No.
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34;
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F83386
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hypothetical protein PA2070 [imported] - Pseudomonas aeruginosa (strain PAO1)
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A;Gene: SGD:HCA4
A;Cross-references: SGD:S0003570; MIPS:YJL033w
A;Map position: 10L
C;Keywords: ATP; nucleotide binding; P-loop
F;85-92/Region: nucleotide-binding motif A (P-l
F;190-195/Region: nucleotide-binding motif B
F;194-197/Region: DEAD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable RNA helicase CA4 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J1250; protein YJL033w
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change
C;Accession: S56805; C34848
R;Pohl, T.M.; Aljinovic, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: B71326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P20448; EMBL:Z49308; NID:g1008154; PIDN:CAA89324.1; PID:g1008 R;Chang, T.H.; Arenas, J.; Abelson, J. R;Chang, T.H.; Arenas, J.; Abelson, J. Proc. Natl. Acad. Sci. U.S.A. 87, 1571-1575, 1990.
A;Title: Identification of five putative yeast RNA helicase genes.
A;Reference number: A34848; MUID:90160368; PMID:2406722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:083444; GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC6541:
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0429
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C;Genetics:
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A; Residues: 192-380, 'I', 382 < CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Pohl, T.M.; Aljinovic, G. submitted to the Protein Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-622 < COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: C34848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-770 <TOV>
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FSAGLVIGGK 151
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Pred. No.
                                                                                                                          Score 39; DB 2;
Pred. No. 1.1e+02
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C;Accession: F83386
C;Accession: F83386
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, Agstover, C.K.; Pham, X.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, A.; Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: F83386
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Experimental source: strain PA01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Balasubramanian, M.K.; Hirani, B.R.; Burke, J.D.; Gould, K.L.
J. Cell Biol. 125, 1289-1301, 1994
A;Title: The Schizosaccharomyces pombe cdc3(+) gene encodes a profilin essential A;Reference number: A53952; MUID:94266961; PMID:8207058
A;Accession: A53952
A;Atctus: preliminary
A;Status: preliminary
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R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, August 1997
A;Reference number: Z21751
A;Accession: T38785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004; Accession: F83386
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-127 <BAL>
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A; Introns: 5/1; 116/1
C; Superfamily: profilin
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AG3578
hypothetical protein BMEII0552 [imported] - Brucella melitensis (strain 16M)
hypothetical protein BMEII0552 [imported] - Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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Alternate names: cdc3 protein
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                           FGTGIILAGQ 67
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Pred. No. 1.5e+02;
1; Mismatches 1;
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28;
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C;Accession: AG3578
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, f. R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, f.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A;Reference number: AD3252; PMID:11756688
A;Recession: AG3578
A;Accession: AG3578
A;Accession: AG3578
A;Besidues: preliminary
A;Cross-references: UNIPROT:Q44701; UNIPROT:Q8FVUO; GB:AE008918; PIDN:AAL53794.1; PID:g1:A;Experimental source: strain 16M
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A;Map po
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 [similarity] - American alligator n C;Species: mitochondrion Alligator mississippiensis (American alligator) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T11285; T43695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, July 1998
A;Description: The complete mitochondrial genome
A;Reference number: 217258
A;Accession: T11285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
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A;Residues: 1-98,'A',100-101,'CYA',105-171 <80R>
A;Cross-references: EMBL:AF069428; PIDN:AAD09992.1; PID:g3219527; GSPDB:GN00134
                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords:
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Best Local
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R;Ito, N.; Tomizawa, K.; Tanaka, K.; Matsui, M.; plant Mol. Biol. 34, 307-316, 1997
A;Title: Characterization of 26S proteasome alfa-
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Best Local S
Matches 8
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6; Conserv
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                                                                                                                                                                                                                                                                                                               Similarity
8; Conserv
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57.1%;
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                                                           Kendrick, R.; Sato, T.; Nakagawa,
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o'Callaghan, D.; Letesso
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26S proteasome alfa-

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A; Molecule type: DNA
A; Residues: 1-272 < STO>
                                                                                                                                                                                                                                                                                                            A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: A8477 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tal euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: A84747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g33560 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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A; Residues: 1-249 <STO>
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Best Loc
Matches
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                                                                                                                          Gene: At2g33560
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Similarity 63.
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Score 38; DB
Pred. No. 59;
3; Mismatches
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Pred. No.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-348 < COH>
A;Cross-references: UNIPROT:065348; EMBL:AF065444; NID:g3153888; PIDN:AAC17441.1;
A;Experimental source: cultivar Sparkle
C;Genetics:
A;Gene: Rit1
C;Superfamily: Arabidopsis thaliana zinc transporter ZIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q8UGB3; GB:AE008688; PIDN:AAL42138.1; PID:g17739523; GSPDB:GNA;Experimental source: strain C58 (Dupont) C;Genetics: C;Genetics: A;Gene: Atul125
A;Gene: Atul125
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.

A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; MUID:21608550; A;Accession: AD2715
hypothetical protein F28A12.4 - Car
C;Species: Caenorhabditis elegans
C;Date: 29-OCt-1999 #sequence_rev
C;Accession: T28954
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A;Title: The role of iron-deficiency stress responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable Fe(II) transport protein, root - garden pea
C;Species: Pisum sativum (garden pea)
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Best Local Similarity
"---hes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L., erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABC transporter, membrane spanning protein Atul125 [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #text_change 09-Jul-2004 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z15642
A; Accession: T06385
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C;Accession: T06385
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A; Residues: 1-298 < KUR >
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58.3%;
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77.8%;
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                                                                   Caenorhabditis elegans
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Pred. No.
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Pred. No.
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                     29-Oct-1999 #text_change
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64;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-389 <SAM's
A;Cess-references: UNIPROT:Q22972; EMBL:U64851; PIDN:AAC47989.1; GSPDB:GN00023; CESP:F2
A;Cross-references: UNIPROT:Q22972; EMBL:U64851; PIDN:AAC47989.1; GSPDB:GN00023; CESP:F2
A;Cross-references: UNIPROT:Q22972; EMBL:U64851; PIDN:AAC47989.1; GSPDB:GN00023; CESP:F2
A;Cenetics: A;Cenetics: Strain Bristol N2; clone F28A12
A;Gene: CESP:F28A12.4
A;Gene: CESP:F28A12.4
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submitted to the EMBL Data Library, July 1996
A,Description: The sequence of C. elegans cosmid F28A12.
A;Reference number: Z20547
A;Accession: T28954
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A;Introns: 104/2; 147/3; 175/3; 258/3; 301/3; 341/3
C;Superfamily: pensin
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T40924
nuclear localization protein - fission yeast (Schizosaccharomyces pombe)
nuclear localization protein - fission yeast (Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40924
C;Accession: T40924
A;Accession: T4
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A; Residues: 1-390 < VOL-
A; Experimental source: strain 972h-; cosmid c1281
A; Experimental source: strain 972h-; cosmid c1281
A; Experimental source: strain 972h-; cosmid c1281
A; Experimental source: strain 972h-; cosmid c1281
A; Experimental source: strain 972h-; cosmid c1281
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Best Local S
Matches 7
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule: 1-494 <KUR>
A;Residues: 1-494 <KUR>
A;Cross-references: UNIPROT:Q8UGB3; GB:AE007869; PIDN:AAK86928.1;
C;Genetics: C;Genetics: C;Genetics: AGR C_2083
A;Map position: circular chromosome
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Local Similarity 58.3%;
Es 7; Conservative
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les 6; Conserv
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EFGARIIVGGR 199
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Pred. No. 83;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB
pred. No. 83;
4; Mismatches
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. 83;
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A;Gene: BME:
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Best Local S
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A;Map position: 1
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7; Conserve
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hypothetical protein T10P12.2 [imported] - Arabidopsis thaliana hypothetical protein T10P12.2 [imported] - Arabidopsis thaliana (Touse-ear cress) c; Species: Arabidopsis thaliana (Touse-ear cress) c; Species: Arabidopsis thaliana (Touse-ear cress) c; Species: Arabidopsis thaliana (Touse-ear cress) c; Species: O2-Mar-2001 #sequence_revision O2-Mar-2001 #text_change 09-Jul-2004 c; Species: O2-Mar-2001 #sequence_revision O2-Mar-2001 #text_change 09-Jul-2004 c; Shuff, C.; Accession: G96498 c; A.; Comm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., R; Theologis, A.; Ecker, J. C.; Conmay, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Conmit, C., Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti, R.; Marziall, A.; Allhors: J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti, R.; Marziall, C.A.; Li, K., Rooney, T.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziall, R.; M.; W., D.; Yu, J.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Roy, W., D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Reference number: A86141; MUID:21016719; pMID:11130712
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Rollvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesscon, Nac. 1. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens) A;Reference number: AD3252; PMID:11756688
A;Accession: AE3463
A;Accession: AE3463
A;Accession: AE3463
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A;Molecule type: DNA
A;Molecule type: CNR
A;Residues: 1-630 «KUR»
A;Experimental source: strain 16M
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-748 <STO>
A;Cross-references: UNIPROT:Q9XIG6; GB:AE005173; NID:g5080761; PIDN:AAD39271.1; GSPDB GN(
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265 OFGSVKVAGGOFL 277
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7; Conserva
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77.8%;
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87.5%;
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; Pred. No. 1e+02;
1; Mismatches 1
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pred. No. 1.3e+02;
1; Mismatches 0;
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Pred. No. 1.5e+02;
                                                                                                                                                                                                           Mismatches
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RESULT 36
D64012
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete 3B0502, MUID:21534947; PMID:11677608
hypothetical protein H10704 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae A;Variety: strain Rd KW20 A;Variety: strain Rd KW20 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: D64011; T09409 C;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1195 <KANS
A;Residues: 1-1195 <KANS
A;Residues: 1-1195 <KANS
A;Residues: 1-1195 <KANS
A;Residues: 1-1195 <KANS
A;Residues: 1-1195 <KANS
A;Rose-farences: UNIPROT:Q55786; EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA1043
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology
C;Keywords: methyltransferase
E;737/Binding site: methylcobalamin cobalt (His) (axial ligand) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997
C;Accession: S76592
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A;Accession: S76592
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
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A; Residues: 1-754 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.; Moule, S.; O'Gaora, P.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: competence protein ComEC
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                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                                                                                                                   EYGAGIVIG
                                                                                                                                                                                                                                                                                                    EFGAGLVLG
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77.8%;
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66.7%;
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Pred. No.
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Pred. No. 1.6e+02;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                          2.4e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                Length 1195;
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  R.A.; Kirkness, E.F.; Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EC 2.1.1.13) [similarity]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  754;
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A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                Gaps
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JS0297
                       A;Experimental source: C;Genetics: A;Gene: lin2445
                                                     A;Residues: 1-181 <GLA>
A;Cross-references: UNIPROT:Q928T7; GB:AL592022; PIDN:CAC97672.1; PID:g16414967; GSPDB:GN
A:Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1737
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Matches
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Gene 81, 237-243, 1989
A;Title: Characterization of an infection structure-specific
A;Reference number: JS0297; MUID:90034196; PMID:2806914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; SA;Title: Whole-genome random sequencing and assembly of Haemophilus A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64012
                                                                                                                                                                                                                                                                                                                                     infection structure-specific protein - rust fungus (Uromyces appendiculatus)
C;Species: Uromyces appendiculatus
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: JS0297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-61 < TIGR>
                                                                                                                                                                                                                                      A; Reference number: JS0297; A; Accession: JS0297
                                                                                                                                                                                                                                                                                                             R; Bhairi, S.M.; Staples, R.C.; Freve,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: HI0704
                                                                                                                                                           C; Comment: This
                                                                                                                                                                           A; Cross-references: UNIPROT: P14777
                                                                                                                                                                                               A; Residues: 1-150 < BHA>
                                                                                                                                                                                                                  A: Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                   C; Accession: JS02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Gocayme, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
                                      Query Match
Best Local S
Matches 7
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                                      Similarity 7; Conserv
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FGAGLVLGGQF 12
                                                                                                                                                           protein is involved
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                          55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.2%;
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                                      Score 37; DB Pred. No. 49; 1; Mismatches
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                                                                                                                                                                                                                                                                                                               P.; Yoder, O.
                                                                                                                                                           development
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7:
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•-
                                                                          Length 150;
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                                        Indels
                                                                                                                                                           of infection
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NADH-dependent FMN reductase homolog lin2445 [imported] -

Listeria innocua

(strain Clip1)

24

FGGGLGIGGGF

34

D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; V. A;Title: Comparative genomics of Listeria species A; Reference number: AB1077; A; Accession: AH1737 A; Molecule type: DNA A;Status: preliminary R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; MUID:21537279; F.; Kurapkat, G.; Maduen rrez, A.; Vazquez-Boland, PMID:11679669 Dussurget, O.; Entian, G.; Madueno, ō, E.; Berche, P.; tian, K.D.; Maitournam, Voss, H.; W Bloecker, Fsihi, H.; Wehland,

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RESULT 40

ABI471
APIA71
APIA71
APIA71
C; Species: Listeria innocua
C; Species: Listeria innocua
C; Species: Listeria innocua
C; Species: APIA71
C; Accession: AE1471
C; Accession: AE1471
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C; Concer, L.M.; Karst., U.
D; Jones, L.M.; Karst., U.
D; Jones, L.M.; Karst., U.
D; Jones, L.M.; Karst., U.
C; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, M.; Tierrez, A.; Vazque
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A72786
C;Accession: A72786
R;Kawarabayasi, Y; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
R; Kawarabayasi, Y.; Mino, Y.; Horikawa, H.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
awa, Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A; Reference number: A72450; MUID: 99310339; pMID: 10382966
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A;Residues: 1-233 <KAW>
A;Residues: 1-233 <KAW>
A;Cross-references: UNIPROT:Q9YFH4; DDBJ:AP000058; NID:g5103388; PIDN:BAA79187.1; PID:g5
A;Experimental source: strain K1
C;Genetics:
C;Genetics:
A;Gene: APE0270
A;Gene: APE0270
C;Superfamily: maltose transport protein malG
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Best Local Similarity
Matches 7; Conserv
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Best Local S
Matches 8
Search completed: December 9, 2004, 09:21:45
Job time : 3.14568 secs
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Best Local S:
Matches 7
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Local Similarity 80.0%;
es 8; Conservation
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                                                                                                                                       159 FGMGLVFGG 167
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milarity 58.3%;
Conservative
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77.8%;
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Pred. No. 59;
2; Mismatches 3; Indels
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pred. No. 75;
0; Mismatches
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pred. No. 83;
0; Mismatches 2
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